

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 1, 2005, 14:32:46 ; Search time 165 Seconds
(without alignments)
246.120 Million cell updates/sec

Title: US-10-027-603-2

Perfect score: 589

Sequence: 1 MRGATRVSMILLVTVSDCA.....CSRFPDGRYCRSMDLKNINP 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	589	100.0	105	3 AAY66745	Aay66745 Membrane-
2	589	100.0	105	3 AAB18453	Aab18453 A human T
3	589	100.0	105	4 AAB70148	Aab70148 Human G p
4	589	100.0	105	4 AAB68427	Aab68427 Amino aci
5	589	100.0	105	4 AAU12406	Aau12406 Human PRO
6	589	100.0	105	4 AAB53096	Aab53096 Human ang
7	589	100.0	105	4 AAB65268	Aab65268 Human PRO
8	589	100.0	105	4 AAB48175	Aab48175 Human PRO
9	589	100.0	105	4 AAB48067	Aab48067 Human ext
10	589	100.0	105	5 AAM50773	Aam50773 Endocrine
11	589	100.0	105	5 AAU83674	Aau83674 Human PRO
12	589	100.0	105	5 AAB884902	Aab884902 Human PRO
13	589	100.0	105	5 AAO15527	Aao15527 Human phy
14	589	100.0	105	5 AAB06308	Aab06308 Human G p
15	589	100.0	105	5 AAE24382	Aae24382 Human pro
16	589	100.0	105	5 AAB95508	Aab95508 Human ang
17	589	100.0	105	6 ABU58083	Abu58083 Human PRO
18	589	100.0	105	6 ABU59161	Abu59161 Novel hum
19	589	100.0	105	6 ABU82673	Abu82673 Human sec
20	589	100.0	105	6 ABO17850	Abo17850 Novel hum
21	589	100.0	105	6 ABU60592	Abu60592 Human sec
22	589	100.0	105	6 ABU80821	Abu80821 Human PRO
23	589	100.0	105	6 ABO33787	Abo33787 Novel hum
24	589	100.0	105	6 ABU13974	Abu13974 Human PRO
25	589	100.0	105	6 ABU08800	Abu08800 Human end

26	589	100.0	105	6 ABU81104	Abu81104 Human PRO
27	589	100.0	105	6 ABU07603	Abu07603 Human ZVE
28	589	100.0	105	6 ABU72559	Abu72559 Novel hum
29	589	100.0	105	6 ABU66804	Abu66804 Human PRO
30	589	100.0	105	6 ABU59885	Abu59885 Novel sec
31	589	100.0	105	6 ABU59308	Abu59308 Human sec
32	589	100.0	105	6 ABO26005	Abo26005 Human PRO
33	589	100.0	105	6 ABO25075	Abo25075 Human sec
34	589	100.0	105	6 ABU82130	Abu82130 Novel hum
35	589	100.0	105	6 ABU59014	Abu59014 Human sec
36	589	100.0	105	6 ABU92392	Abu92392 Novel hum
37	589	100.0	105	6 ABU59457	Abu59457 Novel hum
38	589	100.0	105	6 ABU67080	Abu67080 Human sec
39	589	100.0	105	6 ABU92223	Abu92223 Novel hum
40	589	100.0	105	6 ABU10929	Abu10929 Human PRO
41	589	100.0	105	6 ABU81681	Abu81681 Novel hum
42	589	100.0	105	6 ABU88620	Abu88620 Human sec
43	589	100.0	105	6 ABO34134	Abo34134 Human PRO
44	589	100.0	105	6 ADA45989	Ada45989 Novel hum
45	589	100.0	105	6 ADA76420	Ada76420 Human PRO

ALIGNMENTS

RESULT 1

AAY66745

ID AAY66745 standard; protein; 105 AA.

XX AC AAY66745;

XX DT 05-APR-2000 (first entry)

XX DE Membrane-bound protein PRO1186.

XX KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;

XX KW pharmaceutical; receptor immunoadhesin; gene mapping.

XX OS Homo sapiens.

XX PN WO9963088-A2.

XX PD 09-DEC-1999.

XX PF 02-JUN-1999; 99WO-US012252.

XX PR 02-JUN-1998; 98US-0087607P.

XX PR 02-JUN-1998; 98US-0087609P.

XX PR 03-JUN-1998; 98US-0087827P.

XX PR 04-JUN-1998; 98US-0088021P.

XX PR 04-JUN-1998; 98US-0088025P.

XX PR 04-JUN-1998; 98US-0088028P.

XX PR 04-JUN-1998; 98US-0088029P.

XX PR 04-JUN-1998; 98US-0088030P.

XX PR 04-JUN-1998; 98US-0088033P.

XX PR 04-JUN-1998; 98US-0088167P.

XX PR 05-JUN-1998; 98US-0088202P.

XX PR 05-JUN-1998; 98US-0088212P.

XX PR 05-JUN-1998; 98US-0088217P.

XX PR 09-JUN-1998; 98US-0088655P.

XX PR 10-JUN-1998; 98US-0088722P.

XX PR 10-JUN-1998; 98US-0088730P.

XX PR 10-JUN-1998; 98US-0088734P.

XX PR 10-JUN-1998; 98US-0088738P.

XX PR 10-JUN-1998; 98US-0088740P.

XX PR 10-JUN-1998; 98US-0088741P.

XX PR 10-JUN-1998; 98US-0088742P.

XX PR 10-JUN-1998; 98US-0088810P.

XX PR 10-JUN-1998; 98US-0088811P.

XX PR 10-JUN-1998; 98US-0088824P.

XX PR 10-JUN-1998; 98US-0088825P.

PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089947P.
PR 19-JUN-1998; 98US-0089948P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 23-JUN-1998; 98US-0090349P.
PR 23-JUN-1998; 98US-0090353P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090431P.
PR 24-JUN-1998; 98US-0090433P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090445P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090472P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090538P.
PR 24-JUN-1998; 98US-0090540P.
PR 24-JUN-1998; 98US-0090557P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090691P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091358P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091519P.
PR 02-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091633P.
PR 02-JUL-1998; 98US-0091646P.
PR 02-JUL-1998; 98US-0091673P.
PR 07-JUL-1998; 98US-0091978P.
PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
PR 04-AUG-1998; 98US-0095301P.
PR 04-AUG-1998; 98US-0095302P.
PR 04-AUG-1998; 98US-0095318P.
PR 04-AUG-1998; 98US-0095321P.
PR 04-AUG-1998; 98US-0095325P.
PR 10-AUG-1998; 98US-0095916P.

PR 10-AUG-1998; 98US-0095929P.
PR 10-AUG-1998; 98US-0096012P.
PR 11-AUG-1998; 98US-0096143P.
PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096329P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096768P.
PR 17-AUG-1998; 98US-0096773P.
PR 17-AUG-1998; 98US-0096791P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096894P.
PR 17-AUG-1998; 98US-0096895P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097951P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.
XX
PA (GETH) GENENTECH INC.

XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;

XX WPI; 2000-072883/06.
XX N-PSDB; AAZ65091.

XX Membrane-bound proteins and related nucleotide sequences.

XX Claim 12; Fig 266; 822pp; English.

XX The invention provides membrane-bound PRO polypeptides and
XX polynucleotides encoding them. The PRO sequences of the invention were
XX identified based on extracellular domain homology screening. The PRO
XX sequences have homology with proteins including LDL receptors, TIE
XX ligands and various enzymes. The membrane-bound proteins and receptor
XX molecules are useful as pharmaceutical and diagnostic agents. Receptor
XX immunoadhesins, for instance, can be used as therapeutic agents to block
XX receptor-ligand interactions. The membrane-bound proteins can also be
XX employed for screening of potential peptide or small molecule inhibitors
XX of the relevant receptor/ligand interaction. The PRO encoding sequences
XX are useful as hybridization probes, in chromosome and gene mapping and in
XX the generation of antisense RNA and DNA. PRO nucleic acid sequences will
XX also be useful for the preparation of PRO polypeptides, especially by
XX recombinant techniques

XX Sequence 105 AA;

XX Query Match 100.0%; Score 589; DB 3; Length 105;

XX Best Local Similarity 100.0%; Pred. No. 3.3e-54;

XX Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGATRVSIMLLLVTSDCAVITGACERDVCGAGTCCCAISLWRLGLMCTPLGRGSEC 60

DB 1 MRGATRVSIMLLLVTSDCAVITGACERDVCGAGTCCCAISLWRLGLMCTPLGRGSEC 60

QY 61 HPGSHKVPFFRKXKHTCPCLNLLCSRPDPGRYRCMDLKNINF 105
 DB 61 HPGSHKVPFFRKXKHTCPCLNLLCSRPDPGRYRCMDLKNINF 105

RESULT 2

AA18453
 ID AAB18453 standard; protein; 105 AA.

XX AC AAB18453;

XX DT 15-JAN-2001 (first entry)

XX DE A human TANGO 266 polypeptide.

XX KW TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267;
 KW cellular proliferation; cellular differentiation; cellular adhesion;
 KW von Willebrand factor-associated disorder; cell trafficking; cancer;
 KW hematopoietic associated disease; atelectasis; pulmonary congestion;
 KW oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
 KW intestinal disorder; spleen associated disease; renal disorder;
 KW cardiovascular disorder; ischemic heart disease; hydrocephalus;
 KW brain herniation; iatrogenic disease; inflammation; meningitis;
 KW Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;
 KW multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..19

FT Protein /note= "signal sequence"

FT Protein /note= "mature protein"

XX PN WO200052022-A1.

XX PD 08-SEP-2000.

XX PF 01-MAR-2000; 2000WO-US005226.

XX PR 01-MAR-1999; 99US-0122458P.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Barnes TM, Holtzman DA, Sharp JD, Fraser CC;

XX DR WPI; 2000-579269/54.

XX DR N-PSDB; AAA75155.

XX PT Novel human and murine secreted proteins designated TANGO 216, 261, 262,
 PT 266 and 267 useful as modulating agents of cellular processes, e.g. for
 PT treating cancer.

XX PS Claim 8; Fig 14; 175pp; English.

XX CC The present sequence represents a human TANGO 266 polypeptide. The
 CC specification also describes TANGO 262, TANGO 216, TANGO 261, and TANGO
 CC 267. The TANGO polypeptides can be used to modulate cellular
 CC proliferation, modulate cellular differentiation and/or modulate cellular
 CC adhesion. The proteins can be used to treat any von Willebrand factor-
 CC associated disorder, regulate extracellular matrix structuring, cellular
 CC adhesion, and cell trafficking and/or migration, modulate cellular
 CC interactions, modulate cell adhesion in proliferative disorders, such as
 CC cancer, modulate the proliferation, differentiation, and/or function of
 CC cells that appear in the bone marrow, and leukocytes, treat bone marrow,
 CC blood and hematopoietic associated diseases and disorders, atelectasis,
 CC pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial
 CC asthma and bronchiectasis, intestinal disorders, spleen associated
 CC diseases, modulate renal disorders, treat cardiovascular disorders such
 CC as ischemic heart disease, modulate the proliferation, differentiation,
 CC and/or function of bone and cartilage cells and to treat bone and/or
 CC cartilage associated diseases or disorder. They may also be used to treat

CC disorders associated with the ovaries, cerebral oedema, hydrocephalus,
 CC brain herniations, iatrogenic disease, inflammations, bacterial and viral
 CC meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's
 CC disease, multiple sclerosis, brain cancers, hydrocephalus and
 CC encephalitis, and treat hepatic disorders

XX SQ Sequence 105 AA;

Query Match 100.0%; Score 589; DB 3; Length 105;

Best Local Similarity 100.0%; Pred. No. 3.3e-54;

Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGRGEEC 60

DB 1 MEGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGRGEEC 60

QY 61 HPGSHKVPFFRKXKHTCPCLNLLCSRPDPGRYRCMDLKNINF 105

DB 61 HPGSHKVPFFRKXKHTCPCLNLLCSRPDPGRYRCMDLKNINF 105

RESULT 3

AAB70148

ID AAB70148 standard; protein; 105 AA.

XX AC AAB70148;

XX DT 29-MAY-2001 (first entry)

XX DE Human G protein-coupled receptor protein-related sequence #4.

XX KW Human; G protein-coupled receptor protein; nootropic; neuroprotective;
 KW hypotensive; orexigenic; antiallergic; antianginal; antimicrobial;
 KW antibacterial; gene therapy; Alzheimer's disease; hypertension; anorexia;
 KW allergy; angina pectoris; infection; MRSA;
 KW multiple resistant Staphylococcus aureus.

XX OS Homo sapiens.

XX PN WO200116309-A1.

XX PD 08-MAR-2001.

XX PF 24-AUG-2000; 2000WO-JP005685.

XX PR 27-AUG-1999; 99JP-00241531.

XX PR 18-JUL-2000; 2000JP-00217474.

XX PA (TAKE) TAKEDA CHEM IND LTD.

XX PI Watanabe T, Terao Y, Shintani Y;

XX DR WPI; 2001-226684/23.

XX PT New human brain-originated guanosine triphosphate protein-coupled
 PT receptor protein, its salt and encoded gene, useful in (gene) diagnosis
 PT and development of preventives and remedies for Alzheimer's disease,
 PT hypertension and anorexia.

XX Example 4; Page 113; 119pp; Japanese.

XX CC The present sequence is provided in a specification relating to a protein
 CC or its salt with an amino acid sequence identical or substantially
 CC similar to a fully defined sequence of 393 amino acids as given in the
 CC specification. The protein is useful in gene diagnosis and development of
 CC preventives and remedies for diseases associated with dysfunction of the
 CC protein, e.g. Alzheimer's disease, hypertension, anorexia, allergy,
 CC angina pectoris and infections (e.g. multiple resistant Staphylococcus
 CC aureus). The proteins and DNA encoding the proteins are also useful for
 CC the treatment of these diseases by gene therapy

XX SQ Sequence 105 AA;

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Query Match      100.0%; Score 589; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.3e-54;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGECC 60
    |||||
Db 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGECC 60
    |||||

QY 61 HPGSHKVPFFFRKRKHHTCPCLPNLLCSRFPDGRYRCSDMLKNINF 105
    |||||
Db 61 HPGSHKVPFFFRKRKHHTCPCLPNLLCSRFPDGRYRCSDMLKNINF 105
    |||||

RESULT 4
AAB68427
ID AAB68427 standard; protein; 105 AA.
XX AC AAB68427;
XX DT 23-JUL-2001 (first entry)
XX DE Amino acid sequence of a human Zven2 polypeptide.
XX KW Zven1; 3p21.1; 3p14.3; Zven2; small cell lung cancer; wound healing;
XX KW antitumour; antiinflammatory; necrosis; tissue growth; digestive enzyme;
XX KW cellular differentiation; gastrointestinal cell contractility;
XX KW gastrointestinal motility; inflammation; hypermotility; diarrhoea;
XX KW Crohn's disease.
XX OS Homo sapiens.
XX PN WO200136465-A2.
XX PD 25-MAY-2001.
XX PF 14-NOV-2000; 2000WO-US031278.
XX PR 16-NOV-1999; 9SUS-00442164.
XX PR 25-FEB-2000; 2000US-00511879.
XX PR 19-APR-2000; 2000US-00552203.
XX PR 07-JUN-2000; 2000US-0210332P.
XX PA (ZYMO ) ZYMOGENETICS INC.
XX PI Sheppard PO, Bishop PD, Whitmore TE, Thompson PP;
XX DR WPI; 2001-355611/37.
XX DR N-PSDB; AAF85427.
XX PT Novel isolated Zven polypeptide useful for inhibiting proliferation of
XX PT tumor cells, for treating small cell cancer of lung, to promote wound
XX PT healing, and for treating Crohn's disease and diarrhea.
XX PS Claim 27; Page 4; 98pp; English.
XX CC The present sequence represents a human Zven2 polypeptide. The
XX CC specification also describes Zven1. The Zven1 gene is present on
XX CC chromosome 3p21.1-3p14.3. The specification also describes Zven2. Zven
XX CC polynucleotides and polypeptides are useful in veterinary and human
XX CC therapeutics, for treating small cell cancer of the lung, to promote
XX CC wound healing, to prevent or to treat an adverse reaction of the skin to
XX CC a skin-sensitizing agent or a skin-irritating agent, to stimulate the
XX CC immune system of an immunocompromised individual, as antitumour agents,
XX CC as antiinflammatory agents, as agents to regulate regeneration or
XX CC remodeling of tissue, as agents to modulate necrosis or tissue growth
XX CC developmental arrest, to inhibit proliferation of tumour cells, cellular
XX CC differentiation and necrosis, to treat disorders associated with
XX CC gastrointestinal cell contractility, secretion of digestive enzymes and
XX CC acids, gastrointestinal motility, recruitment of digestive enzymes,
XX CC inflammation, and conditions associated with hypermotility such as
XX CC diarrhoea and Crohn's disease
XX SQ Sequence 105 AA;
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Query Match      100.0%; Score 589; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.3e-54;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGECC 60
    |||||
Db 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGECC 60
    |||||

QY 61 HPGSHKVPFFFRKRKHHTCPCLPNLLCSRFPDGRYRCSDMLKNINF 105
    |||||
Db 61 HPGSHKVPFFFRKRKHHTCPCLPNLLCSRFPDGRYRCSDMLKNINF 105
    |||||

RESULT 5
AAU12406
ID AAU12406 standard; protein; 105 AA.
XX AC AAU12406;
XX DT 24-OCT-2001 (first entry)
XX DE Human PRO1186 polypeptide sequence.
XX KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
XX KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
XX KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
XX KW A-peptide; factor VIIA; gene therapy.
XX OS Homo sapiens.
XX PN WO200140466-A2.
XX PD 07-JUN-2001.
XX PF 01-DEC-2000; 2000WO-US032678.
XX PR 01-DEC-1999; 99WO-US028301.
XX PR 01-DEC-1999; 99WO-US028634.
XX PR 02-DEC-1999; 99WO-US028551.
XX PR 02-DEC-1999; 99WO-US028564.
XX PR 02-DEC-1999; 99WO-US028565.
XX PR 09-DEC-1999; 99US-0170262P.
XX PR 16-DEC-1999; 99WO-US030095.
XX PR 20-DEC-1999; 99WO-US030311.
XX PR 20-DEC-1999; 99WO-US030999.
XX PR 30-DEC-1999; 99WO-US031243.
XX PR 30-DEC-1999; 99WO-US031274.
XX PR 05-JAN-2000; 2000WO-US000219.
XX PR 06-JAN-2000; 2000WO-US000277.
XX PR 06-JAN-2000; 2000WO-US000376.
XX PR 11-FEB-2000; 2000WO-US003565.
XX PR 18-FEB-2000; 2000WO-US004341.
XX PR 18-FEB-2000; 2000WO-US004342.
XX PR 22-FEB-2000; 2000WO-US004414.
XX PR 24-FEB-2000; 2000WO-US004914.
XX PR 24-FEB-2000; 2000WO-US005004.
XX PR 01-MAR-2000; 2000WO-US005601.
XX PR 02-MAR-2000; 2000WO-US005841.
XX PR 03-MAR-2000; 2000US-0187202P.
XX PR 10-MAR-2000; 2000WO-US006319.
XX PR 15-MAR-2000; 2000WO-US006884.
XX PR 21-MAR-2000; 2000WO-US007377.
XX PR 21-MAR-2000; 2000WO-US007532.
XX PR 30-MAR-2000; 2000WO-US008439.
XX PR 17-MAY-2000; 2000WO-US013705.
XX PR 22-MAY-2000; 2000WO-US014042.
XX PR 30-MAY-2000; 2000WO-US014941.
XX PR 02-JUN-2000; 2000WO-US015264.
XX PR 05-JUN-2000; 2000US-0209832P.
XX PR 28-JUL-2000; 2000WO-US020710.
XX PR 11-AUG-2000; 2000WO-US022031.
XX PR 23-AUG-2000; 2000WO-US023522.
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PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PA (GETH ) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Deenoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2001-408281/43.
XX N-PSDB; AAS21478.
XX
XX Isolated , secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT breast, prostate, cervical.
XX
XX Claim 12; Fig 470; 813pp; English.
XX
XX AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO
CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC differentiation of chondrocytes, the proliferation or gene expression in
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VIIa. The PRO polypeptides can be used in assays to identify molecules
CC involved in binding interactions. The polynucleotides encoding PRO
CC polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy
XX
XX Sequence 105 AA;
XX
XX Query Match 100.0%; Score 589; DB 4; Length 105;
XX Best Local Similarity 100.0%; Pred. NO. 3.3e-54;
XX Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MRGATRVSIIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEC 60
XX |||||
XX DB 1 MRGATRVSIIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEC 60
XX |||||
XX QY 61 HPGSHKVPFFRKXKHTCTCLPNLLCSRPFDGRYRCSMDLKNINF 105
XX |||||
XX DB 61 HPGSHKVPFFRKXKHTCTCLPNLLCSRPFDGRYRCSMDLKNINF 105
XX |||||
XX
XX RESULT 6
XX AAB53096
XX ID AAB53096 standard; protein; 105 AA.
XX AC AAB53096;
XX
XX 28-FEB-2001 (first entry)
XX
XX Human angiogenesis-associated protein PRO1186, SEQ ID NO:165.
XX
XX Human; angiogenesis-associated protein; PRO; endothelial cell growth;
XX cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
XX angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
XX myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
XX Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
XX Alzheimer's disease; Huntington's disease; stroke; drug screening;
XX gene therapy; transgenic animal.
XX
XX Homo sapiens.
XX WO200053753-A2.
XX
XX 14-SEP-2000.
XX
XX 05-JAN-2000; 2000WO-US000219.
XX
XX 08-MAR-1999; 99WO-US005028.
XX 12-MAR-1999; 99US-0123957P.
XX 14-MAY-1999; 99US-0134287P.
XX 02-JUN-1999; 99WO-US012252.
XX 23-JUN-1999; 99US-0141037P.
XX 20-JUL-1999; 99US-0144758P.
XX 26-JUL-1999; 99US-0145698P.
XX 01-SEP-1999; 99WO-US020111.
XX 08-SEP-1999; 99WO-US020594.
XX 15-SEP-1999; 99WO-US021090.
XX 15-SEP-1999; 99WO-US021547.
XX 05-OCT-1999; 99WO-US023089.
XX 30-NOV-1999; 99WO-US028313.
XX 30-NOV-1999; 99WO-US028409.
XX 02-DEC-1999; 99WO-US028564.
XX 02-DEC-1999; 99WO-US028565.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;
PI Paoni NF, Picti RM, Watanabe CK, Williams PM, Wood WI;
XX
XX WPI; 2001-090793/10.
XX N-PSDB; AAC97496.
XX
XX New isolated nucleic acid for producing a PRO polypeptide, analyzing
PT genetic disorders and treating cardiovascular, endothelial or angiogenic
PT disorders, such as atherosclerosis, wounds or cancer.
XX
XX Claim 69; Fig 66; 293pp; English.
XX
XX The invention relates to novel human angiogenesis-associated proteins
CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
CC PRO proteins. The invention also relates to vectors and host cells
CC comprising a PRO nucleic acid, the recombinant production of a PRO
CC protein, PRO antibodies specific for a PRO protein, fusion proteins
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and
CC compounds which inhibit the expression of a PRO gene. The invention
CC additionally encompasses methods of identifying modulators of PRO
CC expression or activity; diagnosing a cardiovascular, endothelial or
CC angiogenic disorder, or a susceptibility to such a disorder by detecting
CC mutations in a PRO gene, or the expression level of a PRO gene within a
CC particular tissue; treating a cardiovascular, endothelial or angiogenic
CC disorder via the administration of a PRO protein, PRO nucleic acid, or
CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
CC administration of a PRO protein, or an agonist or antagonist thereof. PRO
CC nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
CC agonists and PRO antagonists may be used as therapeutic agents to treat
CC cardiovascular, endothelial or angiogenic disorders, such as
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, Huntington's
CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's
CC disease, or stroke. PRO nucleic acids are additionally useful in the
CC recombinant production of PRO proteins, as hybridisation probes to screen
CC libraries to isolate cDNAs with sequence identity to PRO proteins, to map
CC genes encoding PRO proteins, to analyse genetic disorders, and in gene
CC therapy. PRO nucleic acids can also be used to produce transgenic animals
CC useful for the development and screening of potential therapeutic agents.
XX The present sequence represents a PRO protein of the invention
XX
XX Sequence 105 AA;

```

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Query Match      100.0%; Score 589; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.3e-54;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWLRLGLRMCTPLGREGEC 60
   |||||
Db 1 MRGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWLRLGLRMCTPLGREGEC 60
   |||||

QY 61 HPGSHKVPFFRRKRHHHTCPLNLLCSRFPDGRYRCSDMLKNINF 105
   |||||
Db 61 HPGSHKVPFFRRKRHHHTCPLNLLCSRFPDGRYRCSDMLKNINF 105
   |||||

RESULT 7
AAB65268
ID AAB65268 standard; protein; 105 AA.
XX
AC AAB65268;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO1186 (UNQ600) protein sequence SEQ ID NO:371.
XX
KW Human; secreted and transmembrane protein; PRO; cytotostatic; cell death;
KW cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay.
XX
OS Homo sapiens.
XX
PN WO200073454-A1.
XX
PD 07-DEC-2000.
XX
PF
PF 30-MAR-2000; 2000WO-US008439.
XX
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PU;
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WT;
PI Zhang Z;
XX
DR WPI; 2001-032160/04.
DR N-PSDB; AAF44237.
XX
XX PRO polynucleotides used to produce polypeptides used to target bioactive

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PT molecules such as toxins, radiolabels or antibodies, to specific cells,
PT to cause targeted cell death.
XX
PS Claim 12; Fig 266; 935pp; English.
XX
CC The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can
CC be used for targeted delivery of bioactive molecules, such as toxins,
CC radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
CC DNA. They may also be used to produce transgenic animals which are used
CC to develop and screen therapeutically useful reagents. The PRO nucleotide
CC and protein sequence can be used for tissue typing and in treating
CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
CC AAF44470 represent PCR primers and hybridisation probes used in the
CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
CC AAB65300 represent human PRO polynucleotide and protein sequences given
CC in the exemplification of the present invention
XX
SQ Sequence 105 AA;

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```

Query Match      100.0%; Score 589; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.3e-54;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWLRLGLRMCTPLGREGEC 60
   |||||
Db 1 MRGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWLRLGLRMCTPLGREGEC 60
   |||||

QY 61 HPGSHKVPFFRRKRHHHTCPLNLLCSRFPDGRYRCSDMLKNINF 105
   |||||
Db 61 HPGSHKVPFFRRKRHHHTCPLNLLCSRFPDGRYRCSDMLKNINF 105
   |||||

RESULT 8
AAB48175
ID AAB48175 standard; protein; 105 AA.
XX
AC AAB48175;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO1186 polypeptide.
XX
KW PRO1186; PRO184; neoplastic; cell growth; tumour; cancer; breast;
KW ovarian; renal; colorectal; uterine; prostate; lung; melanoma;
KW central nervous system; leukemia; antitumor; cytostatic.
XX
OS Homo sapiens.
XX

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Key      Location/Qualifiers
Peptide  1..19
         /note= "signal sequence"
Protein  20..105
         /note= "mature protein"
Modified-site 33..39
              /note= "N-myristoylation site"
Modified-site 35..41
              /note= "N-myristoylation site"
Modified-site 46..52
              /note= "N-myristoylation site"
Modified-site 88..95
              /note= "tyrosine kinase phosphorylation site"

WO2000075327-A1.
14-DEC-2000.
24-FEB-2000; 2000WO-US004914.
02-JUN-1999; 99WO-US012252.
26-JUL-1999; 99US-0145698P.

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PR 05-JAN-2000; 2000WO-US000219.
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Hillan KJ, Napier MA, Watanabe CK, Wood WI;
XX WPI; 2001-071078/08.
DR N-PSDB; AAC84469.
XX
XX Compositions for inhibiting neoplastic cell growth and treating tumor, a
XX cancer, comprises novel PRO1186 or PRO184 polypeptides or its agonist.
XX Claim 31; Fig 2; 104pp; English.
XX
XX The invention provides PRO1186 and PRO184 polypeptides that can be used
XX for the inhibition of neoplastic cell growth and for treating tumours.
XX The PRO polypeptides can be expressed by standard recombinant
XX methodology. The PRO polypeptides or their agonists are useful for
XX inhibition of neoplastic cell growth and for treating tumours, cancers
XX such as breast, ovarian, renal, colorectal, uterine, prostate, lung,
XX bladder or central nervous system cancers or melanoma and leukemia. The
XX present sequence represents the human PRO1186 polypeptide (encoding cDNA
XX clone ID: DNA60621-1516)
XX
XX Sequence 105 AA;
XX
XX Query Match 100.0%; Score 589; DB 4; Length 105;
XX Best Local Similarity 100.0%; Pred. No. 3.3e-54;
XX Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MEGATRVSIIMLLVTVSDCAVITGACERDVQCAGTCCCAISLWRLGLRMCTPLGREGEC 60
DB 1 MEGATRVSIIMLLVTVSDCAVITGACERDVQCAGTCCCAISLWRLGLRMCTPLGREGEC 60
QY 61 HPGSHKVPFFRRKRKHHTCPLNLLCSRPDPGRYCSMDLKNINF 105
DB 61 HPGSHKVPFFRRKRKHHTCPLNLLCSRPDPGRYCSMDLKNINF 105
XX
XX RESULT 9
XX AAB48067
XX ID AAB48067 standard; protein; 105 AA.
XX AC AAB48067;
XX
XX 19-MAR-2001 (first entry)
XX
XX Human extracellular signaling molecule (EXCS) (ID 2006548CD1).
XX
XX Extracellular signaling molecule; EXCS; anti-inflammatory; human;
XX immunosuppressive; cytostatic; neuroprotective; gastrointestinal;
XX viricide; antibacterial; anti-HIV; human immunodeficiency virus;
XX antifertility; cerebroprotective; nootropic; antiulcer; antifungal;
XX anticonvulsant; tranquilizer; neuroleptic; vasotropic; gynecological;
XX keratolytic; protozoacide; gene therapy.
XX
XX Homo sapiens.
XX
XX WO200070049-A2.
XX
XX 23-NOV-2000.
XX
XX 19-MAY-2000; 2000WO-US013975.
XX
XX 19-MAY-1999; 99US-0134949P.
XX 15-JUL-1999; 99US-0144270P.
XX 30-JUL-1999; 99US-0146700P.
XX 04-OCT-1999; 99US-0157508P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Tang YT, Yue H, Lal P, Burford N, Bandman O, Baughn MR;
XX Azimzai Y, Lu DAM, Patterson C;
XX

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XX WPI; 2001-025021/03.
DR N-PSDB; AAC84303.
XX
XX New human extracellular signaling nucleic acids and polypeptides useful
XX for diagnosing, treating and preventing infections and gastrointestinal,
XX neurological, reproductive, and autoimmune/inflammatory disorders.
XX Claim 1; Page 89; 114pp; English.
XX
XX The invention provides human extracellular signaling molecules (EXCS) and
XX polynucleotides which identify and encode EXCS. EXCS can be expressed by
XX standard recombinant methodology. The amino acid and nucleic acid
XX sequences of EXCS are useful for diagnosing, treating and preventing
XX infections and gastrointestinal (peptic ulcer, dysphagia, pancreatitis),
XX neurological (e.g. epilepsy, ischemic cerebrovascular disease, stroke),
XX reproductive (infertility, ovulatory defects, endometriosis), autoimmune
XX /inflammatory (actinic keratosis, acquired immunodeficiency syndrome
XX (AIDS), Addison's disease), and cell proliferative disorders including
XX cancers (of the breast, adrenal gland, bone). They may also be used to
XX treat fatal familial insomnia, nutritional and metabolic diseases of the
XX nervous system, myopathies, mental disorders (anxiety, schizophrenia,
XX mood), as well as infections caused by parasites (malaria, leishmania,
XX trypanosoma), viral (adenovirus, coronavirus, flavivirus), bacterial
XX (e.g. pneumococcus, staphylococcus, bacillus), and fungal (aspergillus,
XX blastomycetes, dermatophytes) agents. The nucleic acids, polypeptides,
XX antagonists, agonists, pharmaceutical compositions, and antibodies may
XX also be used for treating or preventing disorders associated with
XX increased or decreased expression or activity of EXCS. EXCS
XX polynucleotides may also be used to detect and quantify gene expression
XX in biopsied tissues in which expression of EXCS may be correlated with
XX the disease, to determine presence or excess expression of EXCS, to
XX monitor regulation of EXCS levels during therapeutic intervention, to
XX detect the presence of associated disorders, as targets in microarray, to
XX generate hybridization probes, and to detect differences in gene
XX sequences among normal, carrier or affected individuals. Antibodies may
XX also be used in diagnosing disorders, in monitoring patients being
XX treated with EXCS agonists, antagonists or inhibitors. Sequences AAB48057
XX -B48082 represent the EXCS of the invention
XX
XX Sequence 105 AA;
XX
XX Query Match 100.0%; Score 589; DB 4; Length 105;
XX Best Local Similarity 100.0%; Pred. No. 3.3e-54;
XX Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MEGATRVSIIMLLVTVSDCAVITGACERDVQCAGTCCCAISLWRLGLRMCTPLGREGEC 60
DB 1 MEGATRVSIIMLLVTVSDCAVITGACERDVQCAGTCCCAISLWRLGLRMCTPLGREGEC 60
QY 61 HPGSHKVPFFRRKRKHHTCPLNLLCSRPDPGRYCSMDLKNINF 105
DB 61 HPGSHKVPFFRRKRKHHTCPLNLLCSRPDPGRYCSMDLKNINF 105
XX
XX RESULT 10
XX AAM50773
XX ID AAM50773 standard; protein; 105 AA.
XX AC AAM50773;
XX
XX 23-APR-2002 (first entry)
XX
XX Endocrine gland-derived vascular endothelial growth factor.
XX
XX Endocrine gland-derived vascular endothelial growth factor; EG-VEGF;
XX human; cell proliferation; cell migration; fenestration;
XX cell differentiation; angiogenesis; chemotaxis; endocrine; infertility;
XX fertility; polycystic ovary syndrome; ovarian cyst; cancer; cytostatic;
XX diagnosis; therapy.
XX
XX Homo sapiens.
XX
XX

```

FH Key Location/Qualifiers
FT 1..19
FT /label= Signal_peptide
FT Protein 20..105
FT /label= Mature_protein
FT Modified-site 33
FT /note= "N-myristoylated"
FT Modified-site 35
FT /note= "N-myristoylated"
FT Modified-site 46
FT /note= "N-myristoylated"
XX WO200200711-A2.
XX 03-JAN-2002.
XX 22-JUN-2001; 2001WO-US020116.
XX 23-JUN-2000; 2000US-0213637P.
PR 07-SEP-2000; 2000US-0230978P.
PR 01-DEC-2000; 2000WO-US032678.
XX (GETH) GENENTECH INC.
XX Ferrara N, Watanabe C, Wood WI;
XX WPI; 2002-130882/17.
DR N-PSDB; ABA91567.
XX New endocrine gland-vascular endothelial growth factor (EG-VEGF)
PT polypeptides, agonists and antagonists, useful for regulating fertility,
PT and for treating cancer of the reproductive organs, e.g. ovarian or
PT prostate cancer.
XX Claim 12; Fig 2; 133pp; English.
XX The present sequence is that of a novel, tissue-restricted, growth and
CC differentiation factor termed endocrine gland-derived vascular
CC endothelial growth factor (EG-VEGF). The sequence is predicted from the
CC open reading frame of a cDNA clone (see ABA91567) obtained from an
CC ovarian tissue library. EG-VEGF induces proliferation, migration and
CC fenestrations in capillary endothelial cells derived from endocrine
CC glands, but has no effect on a variety of other endothelial and non-
CC endothelial cell types tested. The EG-VEGF precursor has a predicted
CC mol.wt. of 11715 and a pI of 9.05. The mature protein (mol.wt. 8600) is
CC cysteine-rich and is predicted to consist of a series of short beta
CC strands with large connecting loops held together by disulfide bonds
CC resulting in a flat fold with finger-like projections that act as
CC interactive surfaces. 80% Homology and 63% identity is shown to venom
CC protein A (VPR) of the black mamba snake, and 76% homology and 58%
CC identity to human protein Bv8. EG-VEGF nucleic acids and polypeptides, as
CC well as agonists and antagonists, can be used in the treatment of
CC conditions associated with hormone-producing tissue, especially ovarian,
CC testicular, cervical, adrenal, placental or prostate tissue. The
CC condition may be polycystic ovary syndrome, cancer, especially ovarian
CC cancer, testicular cancer, prostate cancer or uterine cancer, or ovarian
CC cyst (all claimed). Fertility can be regulated using an EG-VEGF
CC antagonist to inhibit follicle maturation or ovulation. Methods are
CC claimed for identifying compounds that modulate EG-VEGF activity,
CC especially the ability to induce phosphorylation of a kinase involved in
CC cell proliferation or survival, to induce chemotaxis, angiogenesis, or
CC cell differentiation, or to induce endothelial cell proliferation
XX Sequence 105 AA;
SQ
Query Match 100.0%; Score 589; DB 5; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.3e-54;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGATRVSIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRLGRLMCTPLRGEGSEC 60
DB 1 MRGATRVSIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRLGRLMCTPLRGEGSEC 60

QY 61 HPGSHKVPFFRRKRKHTCTCLPNLCSRFPDGRVRCSDMLKNINF 105
DB 61 HPGSHKVPFFRRKRKHTCTCLPNLCSRFPDGRVRCSDMLKNINF 105
RESULT 11
AAU83674
ID AAU83674 standard; protein; 105 AA.
XX AC AAU83674;
XX 08-MAY-2002 (first entry)
XX Human PRO protein, Seq ID No 166.
DE Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha.
XX Homo sapiens.
XX WO200208288-A2.
XX 31-JAN-2002.
XX 29-JUN-2001; 2001WO-US021066.
XX 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220585P.
PR 25-JUL-2000; 2000US-0220605P.
PR 25-JUL-2000; 2000US-0220607P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220638P.
PR 25-JUL-2000; 2000US-0220664P.
PR 25-JUL-2000; 2000US-0220666P.
PR 26-JUL-2000; 2000US-0220893P.
PR 28-JUL-2000; 2000WO-US020710.
PR 01-AUG-2000; 2000US-0222425P.
PR 22-AUG-2000; 2000US-0227113P.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 28-NOV-2000; 2000US-0253646P.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
XX (GETH) GENENTECH INC.
XX Baker KP, Desnoyers L, Gerritsen MB, Goddard A, Godowski PJ;
XX Gramaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2002-172001/22.
XX N-PSDB; ASK33618.
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumors such
PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
PT or liver tumor.
XX Claim 11; Fig 166; 359pp; English.
XX The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC

CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor- α from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. AA083592-AA083713 represent human PRO
 CC protein sequences of the invention
 XX

Sequence 105 AA;

Query Match 100.0%; Score 589; DB 5; Length 105;
 Best Local Similarity 100.0%; Pred. No. 3.3e-54;
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGATRVSIIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGLRMCTPLGREGEC 60
 DB 1 MEGATRVSIIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGLRMCTPLGREGEC 60
 QY 61 HPGSHKVPFFRKXKHTCPCPLNLLCSRPDPGRYRCMDLKNINF 105
 DB 61 HPGSHKVPFFRKXKHTCPCPLNLLCSRPDPGRYRCMDLKNINF 105

RESULT 12

ID ABB84902 standard; protein; 105 AA.

AC ABB84902;

DT 16-MAY-2002 (first entry)

DE Human PRO1186 protein sequence SEQ ID NO:172.

KW Human; angiogenesis; cardiac; cystostatic; antiangiogenic; hypotensive;
 KW vulnerability; antiarteriosclerotic; PRO-agonist; PRO-antagonist; trauma;
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW age-related macular degeneration; arterial restenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping.

OS Homo sapiens.

PN WO200200690-A2.

XX 03-JAN-2002.

XX 20-JUN-2001; 2001WO-US019692.

XX 23-JUN-2000; 2000US-0213637P.

XX 20-JUL-2000; 2000US-0219556P.

XX 25-JUL-2000; 2000US-0220624P.

XX 25-JUL-2000; 2000US-0220664P.

XX 28-JUL-2000; 2000WO-US020710.

XX 02-AUG-2000; 2000US-0222695P.

XX 17-AUG-2000; 2000US-00643657.

XX 23-AUG-2000; 2000WO-US023522.

XX 24-AUG-2000; 2000WO-US023328.

XX 07-SEP-2000; 2000US-0230978P.

XX 18-SEP-2000; 2000US-00664610.

XX 18-SEP-2000; 2000US-00665350.

XX 24-OCT-2000; 2000US-0242922P.

PR 20-DEC-2000; 2000WO-US034956.
 PR 22-JAN-2001; 2001US-00767609.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001US-00866034.
 PR 30-MAY-2001; 2001WO-US017092.
 PR 30-MAY-2001; 2001US-00870574.
 PR 01-JUN-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.

(GETH) GENENTECH INC.

XX Baker KP, Ferrata N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX WPI; 2002-090516/12.

XX N-PSDB; ABL88157.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.

XX Claim 11; Fig 172; 565pp; English.

XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cystostatic,
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
 CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The PRO polynucleotides have applications in molecular biology,
 CC including use as hybridisation probes, and in chromosome and gene
 CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
 CC exemplification of the present invention

XX Sequence 105 AA;

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 Best Local Similarity 100.0%; Pred. No. 3.3e-54;
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 DB 1 MEGATRVSIIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGLRMCTPLGREGEC 60

QY 61 HPGSHKVPFFRKXKHTCPCPLNLLCSRPDPGRYRCMDLKNINF 105

DB 61 HPGSHKVPFFRKXKHTCPCPLNLLCSRPDPGRYRCMDLKNINF 105

RESULT 13

ID AAO15527 standard; protein; 105 AA.

XX AAO15527;

XX 24-OCT-2002 (first entry)

XX Human physiologically-active ZAQ ligand-related protein 3.

XX

```

KW Human; ZAQ ligand; physiologically-active ZAQ ligand; digestive disease;
KW colitis; diarrhoea.
XX
OS Homo sapiens.
XX
PN WO200257443-A1.
XX
PD 25-JUL-2002.
XX
PF 21-JAN-2002; 2002WO-JP000378.
XX
PR 22-JAN-2001; 2001JP-00013027.
XX
PR 17-MAY-2001; 2001JP-00147759.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Yamada T, Suenaga M, Nishimura O;
XX
DR WPI; 2002-566801/60.
XX
PT Industrial production of physiologically-active ZAQ ligand by expressing
PT in transformant prokaryote and refolding in redox buffer, for use in
PT preventing or treating digestive diseases e.g. colitis and diarrhoea.
XX
PS Example 3; Page 76-77; 93pp; Japanese.
XX
CC The invention comprises a method for producing an active peptide that has
CC the same activity as a ZAQ ligand isolated from eukaryotic cells. The
CC method of the invention is useful for the production of a physiologically
CC -active ZAQ ligand for use in preventing or treating digestive diseases
CC (e.g. colitis and diarrhoea). The present amino acid sequence represents a
CC human physiologically active ZAQ ligand-related protein
XX
SQ Sequence 105 AA;
Query Match 100.0%; Score 589; DB 5; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.3e-54;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGEC 60
DB 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGEC 60
QY 61 HPGSHKVPFFRRKRKHTCPCLPNLLCSRFPPDGRYRCSMDLKNINF 105
DB 61 HPGSHKVPFFRRKRKHTCPCLPNLLCSRFPPDGRYRCSMDLKNINF 105
RESULT 14
ABB06308
ID ABB06308 standard; protein; 105 AA.
XX
AC ABB06308;
XX
DT 27-MAY-2002 (first entry)
XX
DE Human G protein-coupled receptor ZAQ ligand protein SEQ ID NO:23.
XX
KW G protein-coupled receptor; ZAQ ligand; physiologically active peptide;
KW ZAQ; antidiarrheic; laxative; drug development; digestive disease;
KW colitis; diarrhoea; constipation; poor-absorption syndrome; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200206483-A1.
XX
PD 24-JAN-2002.
XX
PF 17-JUL-2001; 2001WO-JP006162.
XX
PR 18-JUL-2000; 2000JP-00217442.
XX
PR 02-FEB-2001; 2001JP-00026779.
XX

PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Ohtaki T, Masuda Y, Takatsu Y, Watanabe T, Terao Y, Shintani Y;
XX
DR WPI; 2002-188546/24.
XX
DR N-PSDB; ABL49637.
XX
PT Physiologically-active peptides from cows milk. useful for developing
PT drugs to treat ZAQ-mediated diseases, particularly digestive diseases
PT like colitis, diarrhoea, constipation and poor-absorption syndrome, by
PT gene therapy.
XX
PS Claim 5; Page 61; 191pp; Japanese.
XX
CC The present invention describes a peptide containing an amino acid
CC sequence (I) identical to or substantially similar to that of the
CC sequences in ABB06305 or ABB06306, or its salt. (I) has antidiarrheic and
CC laxative activities. The peptides and encoding DNAs from the present
CC invention are useful for developing drugs to treat digestive diseases
CC like colitis, diarrhoea, constipation and poor-absorption syndrome,
CC including gene therapy. The physiologically-active cows milk-originated
CC peptides are applicable as a specific ligand of brain-originated orphan G
CC protein-coupled receptor protein ZAQ. ABL49615 to ABB40659 and ABB06303
CC to ABB06315 represent sequences used in the exemplification of the
CC present invention
XX
SQ Sequence 105 AA;
Query Match 100.0%; Score 589; DB 5; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.3e-54;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGEC 60
DB 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGEC 60
QY 61 HPGSHKVPFFRRKRKHTCPCLPNLLCSRFPPDGRYRCSMDLKNINF 105
DB 61 HPGSHKVPFFRRKRKHTCPCLPNLLCSRFPPDGRYRCSMDLKNINF 105
RESULT 15
AAE24382
ID AAE24382 standard; protein; 105 AA.
XX
AC AAE24382;
XX
DT 04-OCT-2002 (first entry)
XX
DE Human prokineticin 1 precursor protein.
XX
KW Human; prokineticin 1; gastrointestinal motility; intestinal cancer;
KW irritable bowel syndrome; gastrointestinal reflux disease; diarrhoea;
KW diabetic gastroparesis; chronic constipation; malabsorptive disorder;
KW inflammatory bowel disorder; analgesic; infectious disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /label= signal_peptide
FT 20..105
FT /note= "Mature human prokineticin 1"
XX
PN WO200236625-A2.
XX
PD 10-MAY-2002.
XX
PF 01-NOV-2001; 2001WO-US047969.
XX
PR 03-NOV-2000; 2000US-0245882P.
XX

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PA (REGC) UNIV CALIFORNIA.

XX
PI Zhou Q, Ehlert FJ;

XX
DR WPI: 2002-479752/51.

XX
DR N-PSDB; AAD39321.

XX
PT New isolated human prokineticin 1 and 2 polypeptides that stimulate
PT gastrointestinal smooth muscle contraction, useful for improving impaired
PT gastrointestinal motility in irritable bowel syndrome, chronic
PT constipation.

XX
PS Example 1; Fig 1; 86pp; English.

XX
CC The invention relates to human prokineticin 1 and 2 polypeptides that
CC stimulate gastrointestinal smooth muscle contraction and nucleic acid
CC molecules encoding such polypeptides. Polypeptides of the invention are
CC useful for treating disorders involving impaired gastrointestinal
CC motility. They are useful for stimulating gastrointestinal motility in
CC disorders such as irritable bowel syndrome, diabetic gastroparesis, post-
CC operational ileus, chronic constipation and gastrointestinal reflux
CC disease. The prokineticin antagonists are useful for inhibiting
CC gastrointestinal motility in conditions of diarrhoea, malabsorptive
CC disorders, inflammatory bowel disorders, infectious diseases and
CC intestinal cancers. The antagonists also act as analgesics. The present
CC sequence is human prokineticin 1 precursor protein

XX
SQ Sequence 105 AA;

Query Match 100.0%; Score 589; DB 5; Length 105;

Best Local Similarity 100.0%; Pred. No. 3.3e-54;

Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEGATRVSIIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGEC 60

Db 1 MEGATRVSIIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGEC 60

Qy 61 HPGSHKVPFFRKRRKHHTCPCLPNLLCSRFPGDGRYRCMDLKNINF 105

Db 61 HPGSHKVPFFRKRRKHHTCPCLPNLLCSRFPGDGRYRCMDLKNINF 105

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Job time : 175 secs

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OM protein - protein search, using sw model

Run on: November 1, 2005, 14:52:11 ; Search time 167 Seconds
(without alignments)
262.841 Million cell updates/sec

Title: US-10-027-603-2

Perfect score: 589

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Searched: 1865214 seqs, 418043040 residues

Total number of hits satisfying chosen parameters: 1865214

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

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- 18: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep.*
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SUMMARIES

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5	589	100.0	105	9	US-09-989-731-371	Sequence 371, App
6	589	100.0	105	9	US-09-989-732-371	Sequence 371, App
7	589	100.0	105	9	US-09-991-073-371	Sequence 371, App
8	589	100.0	105	9	US-09-990-442-371	Sequence 371, App
9	589	100.0	105	9	US-09-991-163-371	Sequence 371, App
10	589	100.0	105	9	US-09-993-604-371	Sequence 371, App
11	589	100.0	105	9	US-09-990-456-371	Sequence 371, App

12	589	100.0	105	9	US-09-989-721-371	Sequence 371, App
13	589	100.0	105	9	US-09-992-598-371	Sequence 371, App
14	589	100.0	105	9	US-09-886-242A-2	Sequence 2, Appli
15	589	100.0	105	9	US-09-989-293A-371	Sequence 11, Appl
16	589	100.0	105	9	US-09-965-528-11	Sequence 371, App
17	589	100.0	105	9	US-09-989-735-371	Sequence 371, App
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33	589	100.0	105	10	US-09-796-753-64	Sequence 64, Appl
34	589	100.0	105	10	US-09-990-711-371	Sequence 371, App
35	589	100.0	105	10	US-09-989-726-371	Sequence 371, App
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ALIGNMENTS

RESULT 1
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; Sequence 371, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumaas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC63
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049786	PRIOR FILING DATE: 1997-06-16
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PRIOR APPLICATION NUMBER: 60/065311	PRIOR FILING DATE: 1997-11-13
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73	PRIOR FILING DATE: 1998-06-25	

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1	MRGATRVISMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRLGRLMCTPLGREGEC	61	HPGSHKVPPFRKRKHTKTCPLPNLLCSRRFPDGRYCSMDLKNINF
60		105	
1	MRGATRVISMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRLGRLMCTPLGREGEC	61	HPGSHKVPPFRKRKHTKTCPLPNLLCSRRFPDGRYCSMDLKNINF
60		105	
<p>Query Match 100.0%; Score 589; DB 9; Length 105; Best Local Similarity 100.0%; Pred. No. 1.4e-53; Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>			
<p>US-09-389-723-371 Sequence 371, Application US/09989723 Patent No. US20020072092A1 GENERAL INFORMATION: APPLICANT: Ashkenazi, Avi J. APPLICANT: Baker, Kevin P. APPLICANT: Botstein, David APPLICANT: Desnoyers, Luc APPLICANT: Eaton, Dan L. APPLICANT: Ferrara, Napoleone APPLICANT: Fong, Sherman APPLICANT: Gerber, Hanspeter APPLICANT: Gerritsen, Mary E. APPLICANT: Goddard, Audrey APPLICANT: Godowski, Paul J. APPLICANT: Grimaldi, J. Christopher APPLICANT: Gurney, Austin L. APPLICANT: Kljavin, Ivar J. APPLICANT: Napier, Mary A. APPLICANT: Pan, James APPLICANT: Paoni, Nicholas F. APPLICANT: Roy, Margaret Ann APPLICANT: Stewart, Timothy A. APPLICANT: Tumas, Daniel APPLICANT: Watanabe, Colin K. APPLICANT: Williams, P. Mickey APPLICANT: Wood, William I. APPLICANT: Zhang, Zemin TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730PIC52 CURRENT APPLICATION NUMBER: US/09/989,723 CURRENT FILING DATE: 2001-11-19 PRIOR APPLICATION NUMBER: 60/049787 PRIOR FILING DATE: 1997-06-16 PRIOR APPLICATION NUMBER: 60/062250</p>			

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? PRIOR FILING DATE: 1998-06-26
? PRIOR APPLICATION NUMBER: 60/091360
? PRIOR FILING DATE: 1998-07-01
? PRIOR APPLICATION NUMBER: 60/091478
? PRIOR FILING DATE: 1998-07-02
? PRIOR APPLICATION NUMBER: 60/091544
? PRIOR FILING DATE: 1998-07-01
? PRIOR APPLICATION NUMBER: 60/091519
? PRIOR FILING DATE: 1998-07-02
? PRIOR APPLICATION NUMBER: 60/091626
? PRIOR FILING DATE: 1998-07-02
? PRIOR APPLICATION NUMBER: 60/091633
? PRIOR FILING DATE: 1998-07-02
? PRIOR APPLICATION NUMBER: 60/091978
? PRIOR FILING DATE: 1998-07-07
? PRIOR APPLICATION NUMBER: 60/091982
? PRIOR FILING DATE: 1998-07-07
? PRIOR APPLICATION NUMBER: 60/092182
? PRIOR FILING DATE: 1998-07-09

Query Match          100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.4e-53;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MGRATRVISMLLVTVSDCAVITGACERDVQCAGTCCALSMLRGURMCTPLGREGEEC 60

Qy 61 HPGSHKVPFPRKRKHTTCPLNLLCSRFPDGRYRCSMDLKNINF 105
Db 61 HPGSHKVPFPRKRKHTTCPLNLLCSRFPDGRYRCSMDLKNINF 105

RESULT 3
US-09-989-279-371
? Sequence 371, Application US/09989279
? Patent No. US20020072496A1
? GENERAL INFORMATION:
? APPLICANT: Ashkenazi, Avi J.
? APPLICANT: Baker, Kevin P.
? APPLICANT: Botstein, David
? APPLICANT: Desnovers, Luc
? APPLICANT: Eaton, Dan L.
? APPLICANT: Ferrara, Napoleone
? APPLICANT: Fong, Sherman
? APPLICANT: Gerber, Hanspeter
? APPLICANT: Gerritsen, Mary E.
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Grimaldi, J. Christopher
? APPLICANT: Gurney, Austin L.
? APPLICANT: Kljavin, Ivar J.
? APPLICANT: Napier, Mary A.
? APPLICANT: Pan, James
? APPLICANT: Paoni, Nicholas F.
? APPLICANT: Roy, Margaret Ann
? APPLICANT: Stewart, Timothy A.
? APPLICANT: Tumas, Daniel
? APPLICANT: Watanabe, Colin K.
? APPLICANT: Williams, P. Mickey
? APPLICANT: Wood, William I.
? APPLICANT: Zhang, Zemin
? TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
? TITLE OF INVENTION: Acids Encoding the Same
? FILE REFERENCE: P2730P1C56
? CURRENT APPLICATION NUMBER: US/09/989,279
? CURRENT FILING DATE: 2001-11-19
? PRIOR APPLICATION NUMBER: 60/049787
? PRIOR FILING DATE: 1997-06-16
? PRIOR APPLICATION NUMBER: 60/062250
? PRIOR FILING DATE: 1997-10-17
? PRIOR APPLICATION NUMBER: 60/065186
? PRIOR FILING DATE: 1997-11-12

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13 PRIOR APPLICATION NUMBER: 60/087106
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146 PRIOR FILING DATE: 1998-07-01

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; PRIOR APPLICATION NUMBER: 60/091478
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; PRIOR APPLICATION NUMBER: 60/091544
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.4e-53;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWLRLMCTPLGREGEC 60
Db      1 MRGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWLRLMCTPLGREGEC 60

Qy      61 HPGSHKVPFFRRKKHHTCPCLPNLLCSRFPDGRYCSMDLKNINF 105
Db      61 HPGSHKVPFFRRKKHHTCPCLPNLLCSRFPDGRYCSMDLKNINF 105

RESULT 4
US-09-989-727-371
; Sequence 371, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC65
; CURRENT APPLICATION NUMBER: US/09/989,727
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
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; PRIOR FILING DATE: 1998-07-01
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; PRIOR APPLICATION NUMBER: 60/091982
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.4e-53;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRMCTPLGREGEC 60
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QY 61 HPGSHKVPFFRRKRKHTCPLNLLCSRPPDGRYRCSMDLKNINF 105
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RESULT 5

US-09-989-731-371
; Sequence 371, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C70
; CURRENT APPLICATION NUMBER: US/09/989,731
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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64	PRIOR APPLICATION NUMBER: 60/091519	
65	PRIOR FILING DATE: 1998-07-02	60/091519
66	PRIOR APPLICATION NUMBER: 60/091519	


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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.4e-53;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 HPGSHKVPFFRRKKHHTCPLNLLCSRFPDGRYCSMDLKNINF 105
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RESULT 6
US-09-989-732-371
; Sequence 371, Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC57
; CURRENT APPLICATION NUMBER: US/09/989,732
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.4e-53;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 HPGSHKVPPFRKRKHTKTCPLNLLCSRRFPDGRYCSMDLKNINF 105

RESULT 7
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; Sequence 371, Application US/09991073
; Patent No. US2002012756A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PLC15
; CURRENT APPLICATION NUMBER: US/09/991,073
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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144 PRIOR FILING DATE: 1998-07-02
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146 PRIOR FILING DATE: 1998-07-02
147 PRIOR APPLICATION NUMBER: 60/091978
148 PRIOR FILING DATE: 1998-07-07

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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.4e-53;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MGRATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRLGLRMCTPLRGEGSEC 60
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QY 61 HPGSHKVPFFRKXKHHTCPCLPNLLCSRPPDGRYRCSMDLKNINF 105
    |||||
Db 61 HPGSHKVPFFRKXKHHTCPCLPNLLCSRPPDGRYRCSMDLKNINF 105
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RESULT 8
US-09-990-442-371
; Sequence 371, Application US/09990442
; Patent No. US20020132252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC8
; CURRENT APPLICATION NUMBER: US/09/990,442
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
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;; PRIOR APPLICATION NUMBER: 60/091982
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;; PRIOR APPLICATION NUMBER: 60/092182

;; PRIOR FILING DATE: 1998-07-09
Query Match 100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.4e-53;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MEGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGRLMCTPLGRGEEC 60

QY 61 HFGSHKVPFFRKXKHTCPCLNLLCSRPDPGRYRCSDMLKNINF 105
DB 61 HFGSHKVPFFRKXKHTCPCLNLLCSRPDPGRYRCSDMLKNINF 105

RESULT 9
US-09-991-163-371
; Sequence 371, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC17
; CURRENT APPLICATION NUMBER: US/09/991,163
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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7	PRIOR FILING DATE: 1998-07-07	
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Query Match 100.0%; Score 589; DB 9; Length 105;

;; PRIOR APPLICATION NUMBER: 60/089948
;; PRIOR FILING DATE: 1998-06-19
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Query Match 100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.4e-53;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 11

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; Sequence 371, Application US/09990456
; Patent No. US20020137890A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC22
; CURRENT APPLICATION NUMBER: US/09/990.456
; CURRENT FILING DATE: 2001-11-14
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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.4e-53;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAIISLWLRGLRMCTPLGREGEC 60
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QY 61 HPGSHKVPFFRKRKHHTCPLNLLCSRFPPDGRYRCSMDLKNINF 105
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Db 61 HPGSHKVPFFRKRKHHTCPLNLLCSRFPPDGRYRCSMDLKNINF 105

RESULT 12

; Sequence 371, Application US/09989721
; Patent No. US20020142961A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC55
; CURRENT APPLICATION NUMBER: US/09/989,721
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1998-07-09

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RESULT 13

US-09-992-598-371
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Patent No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC20
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CURRENT FILING DATE: 2001-11-14
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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RESULT 14
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; Patent No. US20020172678A1
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: EG-VEGF NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: GENENT.1516A
; CURRENT APPLICATION NUMBER: US/09/886,242A
; CURRENT FILING DATE: 2001-06-20
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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Grimaldi, J. Christopher
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Query Match 100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.4e-53;
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Job time : 173 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

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Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.5	17.1	350	JC7188	REIC protein - hum
2	88.5	15.0	640	T08179	LRG5 protein - Chl
3	83	14.1	1101	T16840	hypothetical prote
4	81	13.8	1964	T09059	notch4 - mouse
5	79	13.4	112	XLHU	colipase precursor
6	77.5	13.2	473	A56175	adhesive plaque pr
7	77	13.1	251	A55035	cysteine-rich prot
8	75.5	12.8	1574	T13954	MEGF6 protein - ra
9	75	12.7	734	JC4861	fertilin beta cha
10	75	12.7	2318	S45306	notch 3 protein -
11	75	12.7	2531	T31070	notch homolog - se
12	74	12.6	112	I51909	colipase precursor
13	74	12.6	1620	T27283	hypothetical prote
14	73	12.4	461	A35356	tumor necrosis fac
15	73	12.4	3075	S14458	laminin alpha-1 ch
16	72.5	12.3	643	T25473	hypothetical prote
17	72.5	12.3	2871	A55567	fibritin I - bovi
18	72.5	12.3	3002	A47221	fibritin I - bovi
19	72	12.2	1639	MMFFB2	laminin gamma-1 ch
20	71.5	12.1	591	I48141	acroganin - guine
21	71.5	12.1	601	B36346	fibulin 1 precursor
22	71.5	12.1	683	C36346	fibulin 1 precursor
23	71.5	12.1	1178	A39804	thrombospondin pre
24	71.5	12.1	1854	T13576	hypothetical prote
25	71	12.1	286	S34665	collagen, cuticula
26	71	12.1	593	1 GHU	granulin precursor
27	70.5	12.0	1847	T18308	probable vitellogen
28	70.5	12.0	2871	A55624	fibritin-1 precursor
29	69.5	11.8	802	T24293	hypothetical prote

30	69.5	11.8	949	2	T24294	hypothetical prote
31	69.5	11.8	2352	1	T30201	Notch homolog prot
32	69.5	11.8	4545	1	S25111	alpha-2-macroglobu
33	69	11.7	2918	2	A54105	fibritin-2 precursor
34	69	11.7	3133	2	S52093	hemocytin - silkwo
35	69	11.7	3712	2	S18253	laminin alpha-1 ch
36	68.5	11.6	728	2	I50719	C-Delta-1 - chicke
37	68.5	11.6	850	2	T14450	serine/threonine k
38	68.5	11.6	884	2	T18649	hypothetical prote
39	68.5	11.6	1172	2	A42587	thrombospondin 2 p
40	68.5	11.6	1376	2	G00043	osteonidogen - hum
41	68	11.5	112	2	A46717	colipase precursor
42	68	11.5	345	2	T25138	hypothetical prote
43	68	11.5	358	2	T25137	hypothetical prote
44	68	11.5	427	1	GQHUN	nerve growth facto
45	68	11.5	547	2	A33901	mannosyl-oligosacc

ALIGNMENTS

RESULT 1

JC7188
REIC protein - human
C:Species: Homo sapiens (man)
C>Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000
C:Accession: JC7188
R:Teugi, T.; Miyazaki, M.; Sakaguchi, M.; Inoue, Y.; Namba, M.
Biochem. Biophys. Res. Commun. 268, 20-24, 2000
A>Title: A REIC gene shows down-regulation in human immortalized cells and human tumor-

A:Reference number: JC7188; MUID:20119095; PMID:10652205
A:Accession: JC7188
A:Molecule type: mRNA
A:Residues: 1-350 <TSU>
A:Cross-references: DBBJ:AB034203

A:Experimental source: heart
C:Comment: This protein is a secreted glycoprotein for head induction in amphibian embryo
C:Genetics:
A:Gene: reic
A:Superfamily: human REIC protein
C:Keywords: cardiac muscle; coiled coil; glycoprotein; heart; tumor

Query Match 17.1%; Score 100.5; DB 2; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.0089;
Matches 26; Conservative 3; Mismatches 29; Indels 11; Gaps 4;

QY 26 CERDVQCGAGTCCATSLWRLGL--RMCTPLGREGGECH-PGSHKVYFFPKRKH-----HT 77
DB 208 CDNRDCQFGGCCAFQ---RGLLPVCTPLPVEGELCHDPASRLDLITWLELPDGLDR 264

QY 78 CCLPLNLLC 86
DB 265 CFCASGLLC 273

RESULT 2

T08179
LRG5 protein - Chlamydomonas reinhardtii
C:Species: Chlamydomonas reinhardtii
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
R:Gloeckner, G.; Beck, C.F.
submitted to the EMBL Data Library, October 1996

A:Description: Molecular characterization of a gene (LRG5) involved in blue light signal
A:Accession: T08179
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-640 <GLQ>
A:Cross-references: UNIPROT:Q96397; EMBL:U73817; NID:g1644369; PID:g1644370
C:Genetics:
A:Gene: LRG5

Query Match 15.0%; Score 88.5; DB 2; Length 640;
Best Local Similarity 31.6%; Pred. No. 0.24; 24; Indels 23; Gaps 4;
Matches 24; Conservative 5; Mismatches 23; Indels 26; Gaps 5;
QY 32 CGAGTCCCAISLWLRLMCTPLRGEGECPGSHKVPFPRKRKHTCPCLPNLLCSRF-- 89
Db 488 CTAGRC---NW-----TCLPMWGSGETWPRPLMTF-----SRTACLPPTPCCSRMLR 533
QY 90 -----PDGRYRCSM 98
Db 534 RWRGWAPGGRWRCSL 549
RESULT 3
T16840
hypothetical protein T10E10.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16840
R:Geisel, C.
submitted to the EMBL Data Library, October 1995
A:Description: The sequence of C. elegans cosmid T10E10.
A:Reference number: Z18588
A:Accession: T16840
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1101 <GET>
A:Cross-references: UNIPROT:Q22378; EMBL:U39644; NID:g1049339; PID:g1049343; PIDN:AAA803
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:T10E10.4
A:Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 7
Query Match 14.1%; Score 83; DB 2; Length 1101;
Best Local Similarity 24.4%; Pred. No. 1.3;
Matches 32; Conservative 9; Mismatches 40; Indels 50; Gaps 6;
QY 13 LVTVSDCAVITCACERDVQCGAGTCCCAISLWLRLG----- 46
Db 749 LMSVORCAMGIG-CPFGQCENGVCVCPMPMCSGSIASSVCGMANSCPIGYICEGRGGCL 807
QY 47 --LRMCTPLGR-----EGEECHPG-----SHKVPFPRKRKHTCPCLPNLLCS 87
Db 808 BPLPLCPNGGRASRCYRGAECPGCGTPLGGCLLSNEPVCPTRSNAVCQSPNNVC- 866
QY 88 RPDGRYRCSM 98
Db 867 --PSGA-SCTM 874
RESULT 4
T09059
notch4 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T09059
R:Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; S
submitted to the EMBL Data Library, October 1997
A:Description: Sequence of the mouse major histocompatibility locus class III region.
A:Reference number: Z16543
A:Accession: T09059
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1964 <ROW>
A:Cross-references: UNIPROT:P31695; EMBL:AF030001; NID:g2564945; PID:g2564947
C:Genetics:
A:Gene: notch4
A:Map position: 17
A:Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 67
1679/3; 1729/1; 1761/3
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
C:Keywords: receptor; signal transduction
F:514-545/Domain: EGF homology <EGF>

Query Match 13.8%; Score 81; DB 2; Length 1964;
Best Local Similarity 30.4%; Pred. No. 3.4;
Matches 24; Conservative 7; Mismatches 22; Indels 26; Gaps 5;
QY 26 CERDVQ-----CGAGTCCCAISLWLRLMCTPLRGEGECPGSHKVPFPRKRKHH 76
Db 188 CERDINECFLEBPGPCPGTSCHTL---GSYQCLCPVQEGEPQC-----KLRKG 233
QY 77 TCP---CLPNLLCSRFDPG 92
Db 234 ACPPGSCILNGGTQQLVPEG 252
RESULT 5
X1HU
colipase precursor [validated] - human
N:Alternate names: procolipase
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 19-May-1995 #text_change 09-Jul-2004
C:Accession: A42568; A33949; A03163
R:Sims, H.F.; Lowe, M.E.
Biochemistry 31, 7120-7125, 1992
A:Title: The human colipase gene: isolation, chromosomal location, and tissue-specific
A:Reference number: A42568; MUID:92353041; PMID:1643046
A:Accession: A42568
A:Molecule type: DNA
A:Residues: 1-112 <SIM>
A:Cross-references: UNIPROT:P04118; GB:M95529; NID:g180842; PIDN:AAB05818.1; PID:g148362
A:Note: sequence extracted from NCBI backbone (NCBIN:110576, NCBIN:110578, NCBIP:110580)
R:Lowe, M.E.; Rosenblum, J.L.; McEwen, P.; Strauss, A.W.
Biochemistry 29, 823-828, 1990
A:Title: Cloning and characterization of the human colipase cDNA.
A:Reference number: A33949; MUID:90248429; PMID:2337598
A:Accession: A33949
A:Molecule type: mRNA
A:Residues: 1-112 <LOW>
A:Cross-references: GB:J02883; NID:g180885; PIDN:AAA52054.1; PID:g180886
A:Note: evidence of partial N-glycosylation, possibly at Asn-43
R:Sternby, B.; Engstrom, A.; Hellman, U.; Vihernt, A.M.; Sternby, N.H.; Borgstrom, B.
Biochim. Biophys. Acta 784, 75-80, 1984
A:Title: The primary sequence of human pancreatic colipase.
A:Reference number: A30652; MUID:84104937; PMID:6691986
A:Accession: A03163
A:Molecule type: protein
A:Residues: 23-108 <STE>
C:Comment: Colipase, a cofactor of triacylglycerol lipase (EC 3.1.1.3), forms a 1:1 stoic
se the enzyme is washed off by bile salts, which are known to have an inhibitory effect
C:Genetics:
A:Gene: GDB:CLPS
A:Cross-references: GDB:127277; OMIM:120105
A:Map position: 6pter-6p21.1
A:Introns: 28/3; 69/3
C:Superfamily: colipase
C:Keywords: lipid digestion; lipid hydrolysis; pancreas
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-22/Domain: amino-terminal propeptide #status predicted <APP>
F:23-108/Product: colipase #status experimental <MAI>
F:109-112/Domain: carboxyl-terminal propeptide #status predicted <CPP>
F:34-104, 40-56, 44-80, 45-78, 66-86/Disulfide bonds: #status predicted
F:69, 72, 75, 76/Binding site: micellar substrate (Lys, Tyr, Tyr) #status predicted
Query Match 13.4%; Score 79; DB 1; Length 112;
Best Local Similarity 28.4%; Pred. No. 0.5;
Matches 31; Conservative 9; Mismatches 45; Indels 24; Gaps 6;
QY 9 IMLLLVTVSDCAVITG-----ACRDRVQCGAGTCCCAISLWLRLMCTPLGRE 56
Db 5 LILLJVALSVAYAPGPRGIINLENGELCVNSAQ-C-KSNCCQHSSAL-GLARCTSMASE 62
QY 57 GEECHPGSHKVPFPRKRKHTCPCLPNLLCSRFDPGRYRCSDMLKXNINF 105
Db 63 NSEC---SVKTLY---GIYKPCPERGLTC----EGDKTIVGSITNTNF 101

RESULT 6
A56175
adhesive plaque protein Mgf2 precursor - Mediterranean mussel
C:Species: Mytilus galloprovincialis (Mediterranean mussel)
C>Date: 27-Apr-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C:Accession: A56175
R:Inoue, K.; Takeuchi, Y.; Miki, D.; Odo, S.
J. Biol. Chem. 270, 6698-6701, 1995
A:Title: Mussel adhesive plaque protein gene is a novel member of epidermal growth factor
A:Reference number: A56175; MUID:95204464; PMID:7896812
A:Accession: A56175
A:Molecule type: mRNA
A:Residues: 1-473 <INO>
A:Cross-references: UNIPROT:Q25464; GB:D43794; NID:g602767; PIDN:BAA07852.1; PID:dl00843
C:Keywords: duplication
F:1-17/Domain: signal sequence #status predicted <SIG>
F:387-419/Domain: EGF homology <EGF1>
F:429-460/Domain: EGF homology <EGF>
F:23,36,43,56,75,382,424,455,468,473/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #
Query Match 13.2%; Score 77.5; DB 2; Length 473;
Best Local Similarity 31.2%; Pred. No. 2.4;
Matches 24; Conservative 11; Mismatches 23; Indels 19; Gaps 7;
QY 26 CERDVOQGAGTCCCAISLWRLGLRMCTPLGREGECH-PGSHKVPFFPRKRKHTC---PCL 81
DB 117 CEKNV-CSNPNC-----KNGKCSPLGKTGYKCTCSGGYTGP---RCEVHACKNPCK 165
QY 82 PNLLCSRFPDGR--YRC 96
DB 166 NKGRC--FPDGTGYRC 180
RESULT 7
A55035
cysteine-rich protein CRP1 - earthworm (Enchytraeus buchholzi)
C:Species: Enchytraeus buchholzi
C>Date: 14-Nov-1994 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: A55035; S45034
R:Willuhn, J.; Schmitt-Wrede, H.P.; Greven, H.; Wunderlich, F.
J. Biol. Chem. 269, 24688-24691, 1994
A:Title: cDNA cloning of a cadmium-inducible mRNA encoding a novel cysteine-rich, non-me
A:Reference number: A55035; MUID:95014230; PMID:7929141
A:Accession: A55035
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-251 <WIL>
A:Cross-references: UNIPROT:Q24774; EMBL:X79344; NID:g488802; PIDN:CAA55899.1; PID:g4888
C:Superfamily: ultra-high-sulfur keratin
Query Match 13.1%; Score 77; DB 2; Length 251;
Best Local Similarity 30.9%; Pred. No. 1.6;
Matches 25; Conservative 7; Mismatches 45; Indels 4; Gaps 3;
QY 17 SDCAVITGACERDVOQGAGTCCCAISLWRLGLRMCTPLGREGECHPGSHKVPFFPRKRKH 76
DB 77 SQCKEKGCKKG--CKEG-CCAPKGVAGSCGSKCKEKGCKGCTKRCGTKCGVE 133
QY 77 TCPCLPNLLCSRFPDGRYRCS 97
DB 134 DCPGSPCKCEK-GDCKVNC 153
RESULT 8
T13954
MEGF6 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13954
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998

A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A:Reference number: Z14126; MUID:98360089; PMID:9693030
A:Accession: T13954
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-1574 <NAK>
A:Cross-references: UNIPROT:088281; EMBL:AB011532; NID:g3449293; PIDN:BAA32462.1; PID:g
A:Experimental source: strain Sprague-Dawley; brain
C:Genetics:
A:Gene: MEGF6
Query Match 12.8%; Score 75.5; DB 2; Length 1574;
Best Local Similarity 28.6%; Pred. No. 10;
Matches 24; Conservative 6; Mismatches 33; Indels 21; Gaps 4;
QY 19 CAVITGAC-----ERDVOQGAGTCCCAISLWRLGLRMCTPLGREGECHPGSHKVPFFRKR 73
DB 755 CHRVTEGCLCPGKGTGDCGAD--CPEGRWGLGCQICACPEHGASCNP----- 801
QY 74 KHHTCPCLPNLLCSRFPDGRYRCS 97
DB 802 ETGTCLCLPFGVGRQCD---TCS 822
RESULT 9
JC4861
fertilin beta chain - human
C:Species: Homo sapiens (man)
C>Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 09-Jul-2004
C:Accession: JC4861
R:Gupta, S.K.; Alves, K.; O'Neil Palladino, L.; Mark, G.E.; Hollis, G.F.
Biochem. Biophys. Res. Commun. 224, 318-326, 1996
A:Title: Molecular cloning of the human fertilin beta subunit.
A:Reference number: JC4861; MUID:96295488; PMID:8702389
A:Accession: JC4861
A:Molecule type: mRNA
A:Residues: 1-734 <GUP>
A:Cross-references: UNIPROT:Q99965; GB:U38805; NID:g4151118; PIDN:AAD04206.1; PID:g4151
C:Comment: This protein is an integral sperm membrane glycoprotein, and plays a role in
C:Superfamily: mouse meltrin alpha; disintegrin homology
C:Keywords: glycoprotein; integrin binding; transmembrane protein
F:382-734/Product: fertilin beta chain #status predicted <NAT>
F:382-467/Domain: disintegrin homology <Dis>
F:448-450/Region: integrin binding #status predicted
F:686-708/Domain: transmembrane #status predicted <TMW>
F:121,219,352,458,565/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 12.7%; Score 75; DB 2; Length 734;
Best Local Similarity 28.8%; Pred. No. 6.1;
Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3;
QY 15 TVSDCAVITGAC-----ERDVOQGAGTCCCAISLWRLGLRMCTPLGREGECHPGSHK 66
DB 401 TEQDCALIGETCDIATCFKAGSNCAGPCCNCLFMSKERMCRP---SFEC-----D 452
QY 67 VPFPRKRKHHTCP 79
DB 453 LPEYCNCGSSASCP 465
RESULT 10
S45306
notch 3 protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S45306
R:Bardeili, M.; Dahlstrand, J.; Lendahl, U.
Mech. Dev. 46, 123-136, 1994
A:Title: The novel Notch homologue mouse Notch 3 lacks specific epidermal growth factor
A:Reference number: S45306; MUID:95001556; PMID:7918097
A:Accession: S45306
A:Status: preliminary
A:Molecule type: mRNA

A;Residues: 1-2318 <LAR>
A;Cross-references: UNIPROT:O61982; EMBL:X74760; NID:G483580; PIDN:CAA52776.1; PID:G48358
A;Superfamily: notch protein; ankyrin repeat homology; EGF homology
F:163-195/Domain: EGF homology <EGF1>
F:174-505/Domain: EGF homology <EGF2>
F:1854-885/Domain: EGF homology <EGF>
F:1839-1871/Domain: ankyrin repeat homology <AN1>
F:1872-1904/Domain: ankyrin repeat homology <AN2>
F:1906-1938/Domain: ankyrin repeat homology <AN3>
F:1939-1971/Domain: ankyrin repeat homology <AN4>
F:1972-2004/Domain: ankyrin repeat homology <AN5>

Query Match 12.7%; Score 75; DB 2; Length 2318;
Best Local Similarity 28.1%; Pred. No. 16;
Matches 25; Conservative 5; Mismatches 25; Indels 34; Gaps 5;

QY 19 CAVITGACERDVQCGAGTCCALSLMLRLGLRMCTPLGREGEEC----- 60
Db 1287 CERVARS-RELQCPVGIPCCQT--ARGPRCACPPGLSGPSCRVSRSASGATNASCASA 1343

QY 61 ---HPGS---HKVPFRKRKHHTCPCLP 82
Db 1344 PCLRGSGCLPVSQSVFFER-----CVCAP 1366

RESULT 11
T31070
notch homolog - sea urchin (Lytechinus variegatus)
C;Species: Lytechinus variegatus (variegated urchin)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
A;Accession: T31070
R;Sherwood, D.R.; McClay, D.R.
Development 124, 3363-3374, 1997
A;Title: Identification and localization of a sea urchin Notch homologue: insights into
A;Reference number: Z20966; MUID:97454256; PMID:9310331
A;Accession: T31070
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-2531 <SHE>
A;Cross-references: EMBL:AF000634; NID:G2570350; PID:G2570351; PIDN:AAB82088.1
A;Superfamily: notch protein; ankyrin repeat homology; EGF homology

Query Match 12.7%; Score 75; DB 2; Length 2531;
Best Local Similarity 29.9%; Pred. No. 17;
Matches 23; Conservative 8; Mismatches 32; Indels 14; Gaps 5;

QY 22 ITGACERDVQCGAGTCCAI--SLWLRLGLRMCTPLGREGECHPGSHKVPFRKRKHHTCP 79
Db 120 VDNVCKLEPCQNGGTCLRTTSLMDYEC-FCTP-ANTGENCTDDNHCV-----SNP 168

QY 80 CLPNLLCSRFDPGRYRC 96
Db 169 CLNGAVCTSSSDG-YSC 184

RESULT 12
I51909
collipase precursor - rat
N;Alternate names: procollipase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
A;Accession: I51909; A34623
R;Payne, R.M.; Sims, H.F.; Jennens, M.L.; Lowe, M.E.
Am. J. Physiol. 266, G914-G921, 1994
A;Title: Rat pancreatic lipase and two related proteins: enzymatic properties and mRNA
A;Reference number: I51909; MUID:94262798; PMID:8203536
A;Accession: I51909
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-112 <PAY>
A;Cross-references: UNIPROT:P17084; GB:M58370; NID:G203504; PIDN:AAA20505.1; PID:G203505
R;Wicker, C.; Puigserver, A.
Biochem. Biophys. Res. Commun. 167, 130-136, 1990

A;Title: Rat pancreatic colipase mRNA: nucleotide sequence of a cDNA clone and nutrition.
A;Reference number: A34623; MUID:90179738; PMID:2125524
A;Accession: A34623
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-17,'V',19-112 <WIC>
A;Cross-references: GB:M33333; NID:G203502; PIDN:AAA40943.1; PID:G203503
A;Superfamily: colipase
C;Keywords: lipid digestion; lipid hydrolysis; pancreas
F:1-17/Domain: signal sequence #status predicted <Sig>
F:18-112/Product: colipase #status predicted <Mat>

Query Match 12.6%; Score 74; DB 2; Length 112;
Best Local Similarity 25.8%; Pred. No. 1.6;
Matches 24; Conservative 10; Mismatches 39; Indels 20; Gaps 4;

QY 6 RVSTMLLVTVSDCAVITG-----ACERDVQCGAGTCCALSLMLRLGLRMCTPL 53
Db 2 KVLVLLVTLVAVAYAAPGRGLFINLEDGEICVNSMQC-KSRCCQHDITL-GIARCTHK 59

QY 54 GREGECHPGSHKVPFRKRKHHTCPCLPNLLC 86
Db 60 AVENSECSPKTLYGIYR-----CPCERGLTC 86

RESULT 13
T27283
hypothetical protein Y64G10A.f - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
A;Accession: T27283
R;Ainscough, R.
submitted to the EMBL Data Library, September 1999
A;Reference number: Z20336
A;Accession: T27283
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-1620 <WIL>
A;Cross-references: EMBL:AL110498; NID:e1542303; PIDN:CAB54471.1; CESP:Y64G10A.f
A;Experimental source: clone Y64G10A
C;Genetics:
A;Gene: CESP:Y64G10A.f
A;Introns: 77/1, 116/1, 198/1, 282/1, 365/1, 425/1, 466/1, 548/1, 559/1, 601/1, 625/1, 71

Query Match 12.6%; Score 74; DB 2; Length 1620;
Best Local Similarity 27.5%; Pred. No. 15;
Matches 22; Conservative 4; Mismatches 16; Indels 38; Gaps 4;

QY 16 VSDCAVITGACERDVQCGAG-----TCCALSLMLRLGLRMCTPLGREGECHPGSHKVP 68
Db 1114 VARCHVTGEC----RCPAGWTGPDQQTSC-----PLGRHGECC----- 1148

QY 69 FFRKRKHHTCPCLPNLLCSR 88
Db 1149 -----RHSCQCSNGASCDCR 1162

RESULT 14
A35356
tumor necrosis factor receptor 2 precursor [validated] - human
N;Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
A;Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K.
Science 248, 1019-1023, 1990
A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular and
A;Reference number: A35356; MUID:90260639; PMID:2160731
A;Accession: A35356
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-461 <SMI>
A;Cross-references: UNIPROT:P20333; GB:M32315; NID:G189185; PIDN:AAA59929.1; PID:G189186

Query Match	12.4%	Score 73;	DB 1;	Length 461;
Best Local Similarity	29.5%	Pred. No.	6.6;	

F:1362-1400/Domain: laminin-type EGF-like homology #status atypical <LE17>
F:1403-1449/Domain: laminin-type EGF-like homology <LE18>
F:1452-1506/Domain: laminin-type EGF-like homology <LE19>
F:1509-1553/Domain: laminin-type EGF-like homology <LE20>
F:1554-2125/Domain: I/II, heptad repeats <DOM2>
F:2116-2120/Region: cell adhesion #status predicted
F:2126-3075/Domain: G <DOMG>
F:2142-2300/Domain: laminin G repeat homology <LG1>
F:2329-2484/Domain: laminin G repeat homology <LG2>
F:2510-2676/Domain: laminin G repeat homology <LG3>
F:2534-2536/Region: cell attachment (R-G-D) motif
F:2739-2888/Domain: laminin G repeat homology <LG4>
F:2916-3073/Domain: laminin G repeat homology <LG5>
F:38,164,555,665,763,801,838,926,952,1045,1407,1579,1596,1678,1689,1717,1804,1894,1
rate (Asn) (covalent) #status predicted
F:297-305/Disulfide bonds: #status predicted

Query Match 12.4%; Score 73; DB 2; Length 3075;
Best Local Similarity 23.0%; Pred. No. 32;
Matches 23; Conservative 10; Mismatches 35; Indels 32; Gaps 4;
QY 19 CAVITGACERDVOCAGTCCALSLMLRGLRMCTPL-----GREGECH-----P 62
Db 1056 CDVVTGHCQCKSKFGGRACDQCGLGYRDFPCVPCDCDLRGTSGDACNLEQGLCGVEET 1115
QY 63 GSHKVPFFFRKRKHTCPCLPNLL---CSRFPDGRYRCSD 99
Db 1116 GA-----CPCKENVFGQCNECREGTFALRAD 1142

Search completed: November 1, 2005, 14:52:45
Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 1, 2005, 14:41:04 ; Search time 177 Seconds
(without alignments)
303.776 Million cell updates/sec

Title: US-10-027-603-2

Perfect score: 589

Sequence: 1 MRGATRVSIMLLLVTVSDCA.....CSRFPDGRYRCMDLKNINF 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03:*

1: uniprot_spmot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	589	100.0	105	1 PRK1_HUMAN	P58294 homo sapien
2	588	99.8	105	2 Q8TC69	Q8tc69 homo sapien
3	545	92.5	105	1 PRK1_RAT	Q8r414 rattus norv
4	432	73.3	81	2 Q8K457	Q8k457 mus musculu
5	318	54.0	108	2 Q863H4	Q863h4 bos taurus
6	310.5	52.7	81	1 VPRA_DENPO	P25687 dendroaspis
7	298.5	50.7	96	2 Q8JFQ0	Q8jfq0 bombina max
8	298	50.6	107	1 PRK2_RAT	Q8r413 rattus norv
9	298	50.6	128	2 Q8G3H5	Q863h5 bos taurus
10	287.5	48.8	96	1 BV8_BOMVA	Q9pw66 bombina var
11	282.5	48.0	129	1 PRK2_HUMAN	Q9hc23 homo sapien
12	277.5	47.1	128	1 PRK2_MOUSE	Q9qxu7 mus musculu
13	277.5	47.1	128	2 Q6V8J7	Q6v8j7 rattus norv
14	274.5	46.6	96	2 Q8JFE6	Q8jfe6 bombina max
15	273.5	46.4	96	2 Q8JFX8	Q8jfx8 bombina max
16	273.5	46.4	96	2 Q8JFY1	Q8jfy1 bombina max
17	269.5	45.8	96	2 Q8AFX9	Q8afx9 bombina max
18	269.5	45.8	96	2 Q8JFY2	Q8jfy2 bombina max
19	266.5	45.2	96	2 Q8JFY2	Q8jfy2 bombina max
20	112	19.0	96	2 Q8VEX3	Q8vux3 gallus gall
21	108.5	18.4	221	2 Q8VEJ3	Q8vej3 mus musculu
22	107.5	18.3	224	1 DKK4_HUMAN	Q9ubt3 homo sapien
23	107.5	18.3	350	1 DKK3_CHICK	Q90839 gallus gall
24	104	17.7	255	2 Q9DDA4	Q9dda4 xenopus lae
25	102	17.3	259	1 DKK2_HUMAN	Q9ubt2 homo sapien
26	101	17.1	259	1 DKK2_MOUSE	Q9gyz8 mus musculu
27	101	17.1	259	2 Q8BFW0	Q8bfw0 m mus muscu
28	101	17.1	272	1 DKX1_MOUSE	O54908 mus musculu
29	101	17.1	272	2 Q8OUL5	Q8oul5 mus musculu
30	100.5	17.1	171	2 O43532	Q43532 homo sapien
31	100.5	17.1	215	2 Q8N294	Q8n294 homo sapien

32	100.5	17.1	350	1 DKK3_HUMAN	Q9ubp4 homo sapien
33	99.5	16.9	277	2 Q9ES33	Q9es33 rattus norv
34	98.5	16.7	349	1 DKK3_MOUSE	Q9qun9 mus musculu
35	97	16.5	266	1 DKX1_HUMAN	O94907 homo sapien
36	96.5	16.4	268	2 Q6PVU5	Q6pvu5 oryctolagus
37	95.5	16.2	259	2 O57464	O57464 xenopus lae
38	94.5	16.0	350	2 Q6PQ81	Q6pq81 homo sapien
39	94	16.0	240	2 Q9FWH3	Q9fwh3 brachydanio
40	90.5	15.4	425	1 CND0_MOUSE	Q8bu04 mus musculu
41	90.5	15.4	425	2 Q642A8	Q642a8 rattus norv
42	88.5	15.0	640	2 Q96397	Q96397 chlamydomon
43	86	14.6	241	2 Q9W6D9	Q9w6d9 brachydanio
44	85	14.4	107	1 COL_RABIT	P42890 oryctolagus
45	83	14.1	708	2 P87363	P87363 gallus gall

ALIGNMENTS

RESULT 1

ID	PRK1_HUMAN	STANDARD;	PRT;	105 AA.
AC	P58294;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	25-JAN-2005 (Rel. 46, Last annotation update)			
DE	Prokineticin 1 precursor (Endocrine-gland-derived vascular endothelial			
DE	growth factor) (EG-VEGF) (Mambakine) (UNQ600/PRO1186).			
GN	Name=PROK1;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21160229; PubMed=11259612;			
RA	Li M., Bullock C.M., Knauer D.J., Ehler F.J., Zhou Q.Y.;			
RT	"Identification of two prokineticin cDNAs: recombinant proteins			
RT	potently contract gastrointestinal smooth muscle.";			
RL	Mol. Pharmacol. 59:692-698(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21419730; PubMed=11528470; DOI=10.1038/35091000;			
RA	LeCouter J., Kowalski J., Foster J., Hass P., Zhang Z.,			
RA	Dillard-Telm L., Frantz G., Rangel L., DeGuzman L., Keller G.-A.,			
RA	Pealle F., Gurney A., Hillan K.J., Ferrara N.;			
RT	"Identification of an angiogenic mitogen selective for endocrine gland			
RT	endothelium.";			
RL	Nature 412:877-884(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Fraser C.;			
RT	"Mambakine, a snake venom related endocrine hormone that controls			
RT	macrophages.";			
RL	Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;			
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,			
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,			
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,			
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,			
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,			
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,			
RA	Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.-H., Yansura D.,			
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,			
RT	"The secreted protein discovery initiative (SPDI), a large-scale			
RT	effort to identify novel human secreted and transmembrane proteins: a			
RT	bioinformatics assessment.";			
RL	Genome Res. 13:2265-2270(2003).			
RN	[5]			
RP	SEQUENCE OF 20-34.			

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RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
CC
CC -!- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle.
CC Induces proliferation, migration and fenestration (the formation
CC of membrane discontinuities) in capillary endothelial cells
CC derived from endocrine glands. Has little or no effect on a
CC variety of other endothelial and non-endothelial cell types.
CC
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed in the steroidogenic glands, ovary,
CC testis, adrenal and placenta.
CC
CC -!- SIMILARITY: Belongs to the prokinectin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to licens@isb-sib.ch).
CC
CC EMBL; AF333024; AAK49918.1; -.
CC EMBL; AY029225; AAK33111.1; -.
CC EMBL; AY358683; AAK09046.1; -.
CC HSSP; P25687; 11MT.
CC Genew; HGNC:18454; PROK1.
CC H-InvDB; HIX0000868; -.
CC MIM; 606233; -.
CC InterPro; IPR009523; Prokinectin.
CC Pfam; PF06607; Prokinectin; 1.
CC Direct protein sequencing; Growth factor; Mitogen; Signal.
KW SIGNAL
FT CHAIN 1 19 Prokinectin 1.
FT DISULFID 20 105 By similarity.
FT DISULFID 26 38 By similarity.
FT DISULFID 32 50 By similarity.
FT DISULFID 37 78 By similarity.
FT DISULFID 60 86 By similarity.
FT DISULFID 80 96 By similarity.
FT DISULFID 96 96 By similarity.
SQ SEQUENCE 105 AA; 11715 MW; C7E3FDE30EFB416A CRC64;

Query Match 100.0%; Score 589; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.9e-52;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGATRVSIMLLLVTSQCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGSEC 60
Db 1 MRGATRVSIMLLLVTSQCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGSEC 60

QY 61 HPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSDMLKNINF 105
Db 61 HPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSDMLKNINF 105

RESULT 2
QSTC69 PRELIMINARY; PRT; 105 AA.
ID Q8TC69
AC Q8TC69;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Prokinectin 1.
GN Name=PROK1;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=restis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=restis;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025399; AAH25399.1; -.
DR HSSP; P25687; 11MT.
DR InterPro; IPR009523; Prokinectin.
DR Pfam; PF06607; Prokinectin; 1.
SQ SEQUENCE 105 AA; 11729 MW; E570FDE30EFB52D2 CRC64;

Query Match 99.8%; Score 588; DB 2; Length 105;
Best Local Similarity 99.0%; Pred. No. 3.7e-52;
Matches 104; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGATRVSIMLLLVTSQCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGSEC 60
Db 1 MRGATRVSIMLLLVTSQCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGSEC 60

QY 61 HPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSDMLKNINF 105
Db 61 HPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSDMLKNINF 105

RESULT 3
PK1_RAT STANDARD; PRT; 105 AA.
ID PK1_RAT
AC Q8R414;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Prokinectin 1 precursor (Endocrine-gland-derived vascular endothelial
DE growth factor) (EG-VEGF).
GN Name=Prok1;
OS Rattus norvegicus (Rat);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=22050031; PubMed=12054613; DOI=10.1016/S0006-291X(02)00239-5;
RA Maeda Y., Takatsu Y., Terao Y., Kumano S., Ishibashi Y., Suenaga M.,
RA Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S.,
RA Inatomi N., Ohtaki T., Onda H., Fujino M.;
RT "Isolation and identification of EG-VEGF/prokinectins as cognate
RT ligands for two orphan G-protein-coupled receptors.";
RL Biochem. Biophys. Res. Commun. 293:396-402(2002).
CC -!- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle.
CC Induces proliferation, migration and fenestration (the formation
CC of membrane discontinuities) in capillary endothelial cells
CC derived from endocrine glands. Has little or no effect on a
CC variety of other endothelial and non-endothelial cell types (By
CC similarity).

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CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- SIMILARITY: Belongs to the prokinectin family.
CC -----
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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CC -----
CC EMBL; AY089983; AA09104.1; -.
CC HSSP; P25687; IIMT.
CC RGD; 620898; Prokl.
CC InterPro; IPR009523; Prokinectin.
CC Pfam; PF06607; Prokinectin; 1.
CC Growth factor; Mitogen; Signal.
CC FT SIGNAL 1 19 Potential.
CC CHAIN 20 105 Prokinectin 1.
CC FT DISULFID 26 38 By similarity.
CC FT DISULFID 32 50 By similarity.
CC FT DISULFID 37 78 By similarity.
CC FT DISULFID 60 86 By similarity.
CC FT DISULFID 80 96 By similarity.
CC SEQUENCE 105 AA; 11642 MW; 8DF0C4212251C5B6 CRC64;
SQ
Query Match 92.5%; Score 545; DB 1; Length 105;
Best Local Similarity 89.5%; Pred. No. 8.6e-48;
Matches 94; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 1 MGRATRVSIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGRGEGRC 60
DB 1 MGRGAVQVFMILLATVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGRGEGRC 60
QY 61 HPGSHKVPFRKXKHTTCLNLLCSRPDPGRYCSMDLKNINF 105
DB 61 HPGSHKIPFRKQKHHTCPSPSLCSRPDPGRYCSMDLKNINF 105
RESULT 4
Q8K457 PRELIMINARY; PRT; 81 AA.
AC Q8K457;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Prokinectin 1 (Fragment).
GN Name=Prokl; Synonyms=Pkl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=2022134; PubMed=12024206; DOI=10.1038/417405a;
RA Cheng M.Y., Bullock F.M., Li C., Lee A.G., Bermak J.C., Belluzzi J.,
RA Weaver D.R., Leslie F.M., Zhou Q.Y.;
RT "Prokinectin 2 transmits the behavioural circadian rhythm of the
RT suprachiasmatic nucleus.";
RL Nature 417:405-410(2002).
DR EMBL; AF487281; AA049573.1; -.
DR HSSP; P25687; IIMT.
DR MGD; MGI:2180370; Prokl.
DR GO; GO:0005576; C:extracellular; IDA.
DR GO; GO:000187; P:activation of MAPK; IDA.
DR GO; GO:0007623; P:circadian rhythm; TAS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR GO; GO:0045765; P:regulation of angiogenesis; IDA.
DR InterPro; IPR009523; Prokinectin.
DR Pfam; PF06607; Prokinectin; 1.
DR NON_TER 1
SQ SEQUENCE 81 AA; 9192 MW; 7BBE3EC6B16A8011 CRC64;
```

```
Query Match 73.3%; Score 432; DB 2; Length 81;
Best Local Similarity 87.7%; Pred. No. 2e-36;
Matches 71; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 25 ACERDVQCGAGTCCCAISLWRLGRLMCTPLGRGEGCHPGSHKVPFRKXKHTTCLNLL 84
DB 1 ACERDIQCGAGTCCCAISLWRLGRLMCTPLGRGEGCHPGSHKIPFLRKQKHHTCPSPSL 60
QY 85 LCSRPDPGRYCSMDLKNINF 105
DB 61 LCSRPDPGRYCSMDLKNINF 81
RESULT 5
Q863H4 PRELIMINARY; PRT; 108 AA.
AC Q863H4;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Bv8/prokinectin 2-like protein splice variant.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22612805; PubMed=12728444; DOI=10.1038/sj.embor.embor830;
RA Kaser A., Winklmayr M., Lepperdinger G., Kreil G.;
RT "The AVIT protein family.";
RL EMBO Rep. 4:469-473(2003).
DR EMBL; AY192558; AAP31907.1; -.
DR HSSP; P25687; IIMT.
DR InterPro; IPR009523; Prokinectin.
DR Pfam; PF06607; Prokinectin; 1.
DR SEQUENCE 108 AA; 11672 MW; C00410399A9B215E CRC64;
Query Match 54.0%; Score 318; DB 2; Length 108;
Best Local Similarity 51.9%; Pred. No. 1e-24;
Matches 54; Conservative 15; Mismatches 27; Indels 8; Gaps 1;
QY 1 MGRATRVSIMLLLV-----TVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTP 52
DB 1 MRSRCARLLLLLLLLPPLLLTPAGDAAVITGACDRDPQCGGMCACAVSLWKSIRICTP 60
QY 53 LGREGEGCHPGSHKVPFRKXKHTTCLNLLCSRPDPGRYRC 96
DB 61 MGKVGDSCHPMTRKVPFLGRMHHTCPCLPLGLACSRTSFNRVTC 104
RESULT 6
VPR4_DENPO STANDARD; PRT; 81 AA.
AC P25687;
DT 01-MAY-1992 (Rel. 22, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Intestinal toxin 1 (MIT 1) (Venom protein A).
OS Dendroaspis polylepis polylepis (Black mamba).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Elapinae; Dendroaspis.
OX NCBI_TaxID=8620;
RN [1]
RP SEQUENCE.
RX MEDLINE=81115818; PubMed=7461607;
RA Joubert F.J., Strydom D.J.;
RT "Snake venom. The amino acid sequence of protein A from Dendroaspis
RT polylepis polylepis (black mamba) venom.";
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RL Hoppe-Seyler's Z. Physiol. Chem. 361:1787-1794 (1980).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=20036442; PubMed=10567694; DOI=10.1016/S0014-5793(99)01459-3;
RA Schweitz H., Pascaud P., Diocot S., Moirier D., Lazdunski M.;
RT "MIT1, a black mamba toxin with a new and highly potent activity on
RT intestinal contraction.";
RL FEBS Lett. 461:183-188 (1998).
RN [3]
RP STRUCTURE BY NMR.
RC TISSUE=Venom;
RA Boisbouvier J., Albrand J.-P., Blackledge M., Jaquinod M.,
RA Schweitz H., Lazdunski M., Marion D.;
RT "A structural homologue of colipase in black mamba venom revealed by
RT NMR floating hololipid bridge analysis.";
RL J. Mol. Biol. 283:205-219 (1998).
CC -!- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the prokinectin family.
DR PDB; 1MT7; NMR; @=1-81.
DR InterPro; IPR009523; Prokinectin.
DR Pfam; PF06607; Prokinectin; 1.
KW 3D-structure; Direct protein sequencing; Toxin.
FT DISULFID 7 19
FT DISULFID 13 31
FT DISULFID 18 60
FT DISULFID 41 68
FT DISULFID 62 78
FT VARIANT 73 73 P -> Q (in protein A').
FT CONFLICT 18 18 C -> S (in Ref. 1).
FT CONFLICT 22 22 S -> C (in Ref. 1).
SQ SEQUENCE 81 AA; 8645 MW; 6C01368841572044 CRC64;

Query Match 52.7%; Score 310.5; DB 1; Length 81;
Best Local Similarity 62.8%; Pred. No. 4.5e-24;
Matches 49; Conservative 14; Mismatches 14; Indels 1; Gaps 1;

QY 20 AVITGACERDVQCGAGTCCATSLWLRLGRLMCTPLRGREGECVPGSHKVPFRKXK-HHTC 78
DB 1 AVITGACERDLQCGGTGTCVAVSLWTKSVRVCTPVGTGDCGHPASHKTFPSGQRKHHTC 60

QY 79 PCLPNLLCSRPDPGRYRC 96
DB 61 PCAPNLACVQTSPPKFKC 78

RESULT 7
QB JFQO PRELIMINARY; PRT; 96 AA.
AC QB JFQO;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Bv8 protein homolog 2.
OS Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=161274;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin secretions;
RX MEDLINE=22515712; PubMed=12628381; DOI=10.1016/S1096-4959(02)00294-4;
RA Lai R., Liu H., Lee W.H., Zhang Y.;
RT "Two novel Bv8-like peptides from skin secretions of the toad Bombina
RT maxima.";
RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 134:509-514 (2003).
DR EMBL; AF411091; AAN03822.1; -.
DR HSSP; P25687; 1INT.
DR InterPro; IPR009523; Prokinectin.
DR Pfam; PF06607; Prokinectin; 1.
SQ SEQUENCE 96 AA; 10198 MW; EC4EAA5EFE49B2F0 CRC64;

Query Match 50.7%; Score 298.5; DB 2; Length 96;
Best Local Similarity 53.6%; Pred. No. 8.8e-23;
Matches 52; Conservative 16; Mismatches 28; Indels 1; Gaps 1;

QY 1 MRGATRVYSIMLLVTVSDCAVITGACERDVQCGAGTCCATSLWLRLGRLMCTPLRGREGEC 60
DB 1 MKCPAQIIVLLLVIAFSHGAVITGACDRDVQCGSGTCCCAASLWSRNIKRVFVPLGNGBEC 60

QY 61 HPGSHKVPFRKXKHTCTCPCLPNLLCSRPDPGRYRC 97
DB 61 HPASHKVPYNGKRLSSLCPCSKSLGTLCKSGE-KFQCS 96

RESULT 8
PK2_RAT STANDARD; PRT; 107 AA.
AC QBR413;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Prokinectin 2 precursor (PK2).
GN Name=Prok2; Synonyms=Bv8;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=22050031; PubMed=12054613; DOI=10.1016/S0006-291X(02)00239-5;
RA Masuda Y., Takatsu Y., Texao Y., Kumano S., Ishibashi Y., Suenaga M.,
RA Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S.,
RA Inatomi N., Ohtaki T., Onda H., Fujino M.;
RT "Isolation and identification of EG-VEGF/prokineticins as cognate
RT ligands for two orphan G-protein-coupled receptors.";
RL Biochem. Biophys. Res. Commun. 293:396-402 (2002).
RN [2]
RP EFFECT ON CIRCADIAN LOCOMOTOR ACTIVITY.
RX MEDLINE=22021234; PubMed=12024206; DOI=10.1038/417405a;
RA Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bernak J.C., Belluzzi J.,
RA Weaver D.R., Leslie F.M., Zhou Q.-Y.;
RT "Prokinectin 2 transmits the behavioural circadian rhythm of the
RT suprachiasmatic nucleus.";
RL Nature 417:405-410 (2002).
CC -!- FUNCTION: May function as an output molecule from the
CC suprachiasmatic nucleus (SCN) that transmits behavioral circadian
CC rhythm. May also function locally within the SCN to synchronize
CC output. Potentially contracts gastrointestinal (GI) smooth muscle (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed at high levels in testis and at
CC lower levels in brain, lung, ovary, spleen, thymus and uterus.
CC -!- INDUCTION: Activated by CLOCK and BMAL1 heterodimers and light;
CC inhibited by period genes (PER1, PER2 and PER3) and cryptochrome
CC genes (CRY1 and CRY2) (Probable).
CC -!- SIMILARITY: Belongs to the prokinectin family.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AY089984; AAM09105.1; -.
DR HSSP; P25687; 1INT.
DR RGD; 620280; Bv8.
DR InterPro; IPR009523; Prokinectin.
DR Pfam; PF06607; Prokinectin; 1.
KW Biological rhythms; Neuropeptide; Signal.
FT SIGNAL 26 Potential.
FT CHAIN 27 107 Prokinectin 2.
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FT DISULFID 33 45 By similarity.
FT DISULFID 39 57 By similarity.
FT DISULFID 44 85 By similarity.
FT DISULFID 67 93 By similarity.
FT DISULFID 87 103 By similarity.
SQ SEQUENCE 107 AA; 11594 MW; BDFP316DCB5PED0 CRC64;

Query Match 50.6%; Score 298; DB 1; Length 107;
Best Local Similarity 54.0%; Pred. No. 1.1e-22;
Matches 47; Conservative 16; Mismatches 24; Indels 0; Gaps 0;

QY 10 MLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGRGECHPGSHKVPF 69
Db 17 LLTTPPAGDAVITGACDKDSQCGGMCACAVSIWKSIRICTPMGQVGDSCPLTRKVPF 76

QY 70 FRKHKHTCPCLPNLLCSRPDPGRYRC 96
Db 77 WGRRHHTCPCLPGLACLRISFNRFC 103

RESULT 9
Q863H5 PRELIMINARY; PRT; 128 AA.
AC Q863H5
DT 01-JUN-2003 (TREMblrel. 24, Created)
DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
DE Bv8/prokineticin 2-like protein.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Testis;
RX MEDLINE=22612805; PubMed=12728244; DOI=10.1038/sj.embor.embor830;
RA Kaser A., Winklmayr M., Lepperdinger G., Kreil G.;
RT "The AVIT protein family."
RL EMBO Rep. 4:469-473(2003).
DR EMBL; AY192557; AAP31906.1; -.
DR HSSP; P25687; IIMT.
DR GO; GO:0005576; C:extracellular; ISS.
DR GO; GO:0001664; F:G-protein-coupled receptor binding; ISS.
DR GO; GO:000187; P:activation of MAPK; ISS.
DR GO; GO:0001525; P:angiogenesis; ISS.
DR GO; GO:0006916; P:anti-apoptosis; ISS.
DR GO; GO:0008283; P:cell proliferation; ISS.
DR GO; GO:0006935; P:chemotaxis; ISS.
DR GO; GO:0007204; P:cytosolic calcium ion concentration elevation; ISS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; ISS.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR GO; GO:0019233; P:perception of pain; ISS.
DR GO; GO:0045987; P:positive regulation of smooth muscle contra. . .; ISS.
DR GO; GO:0007283; P:spermatogenesis; ISS.
DR InterPro; IPR009523; Prokineticin.
DR Pfam; PF06607; Prokineticin; 1.
SQ SEQUENCE 128 AA; 14290 MW; C22CDBDBE40483EC CRC64;

Query Match 50.6%; Score 298; DB 2; Length 128;
Best Local Similarity 43.5%; Pred. No. 1.3e-22;
Matches 54; Conservative 15; Mismatches 27; Indels 28; Gaps 2;

QY 1 MRGATRVISMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTP 52
Db 1 MRSSRCARILLILLPPLLTPAGDAVITGACDRDPQCGGMCACAVSLWKSIRICTP 60

QY 53 LGREGECHPGSH-----KVPFFRKRKHHTCPCLPNLLCSRPDPG 92
Db 61 MGKVGDSCHPMTRIKNHFGNGROERRKRKRKKKVPFLGRMHHTCPCLPGLACRSF 120

QY 93 RYRC 96
|||
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Db 121 RYTC 124

RESULT 10
BV8_BOMVA STANDARD; PRT; 96 AA.
AC Q9PW66;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Protein Bv8 precursor.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=99349621; PubMed=10422759; DOI=10.1016/S0014-2999(99)00229-0;
RA Mollay C., Wechselberger C., Mignogna G., Negri L., Meichiorri P.,
RA Barra D., Kreil G.;
RT venom induce hyperalgesia in rats.;
RL Eur. J. Pharmacol. 374:189-196(1999).
CC -!- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the prokineticin family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC EMBL; AF168790; AAD45816.1; -.
DR HSSP; P25687; IIMT.
DR InterPro; IPR009523; Prokineticin.
DR Pfam; PF06607; Prokineticin; 1.
KW Direct protein sequencing; Signal.
FT SIGNAL 1 19
FT CHAIN 20 96 Protein Bv8.
FT DISULFID 26 38 By similarity.
FT DISULFID 32 50 By similarity.
FT DISULFID 37 78 By similarity.
FT DISULFID 60 86 By similarity.
FT DISULFID 80 95 By similarity.
SQ SEQUENCE 96 AA; 10102 MW; A12490A7437609B4 CRC64;

Query Match 48.8%; Score 287.5; DB 1; Length 96;
Best Local Similarity 50.5%; Pred. No. 1.2e-21;
Matches 49; Conservative 18; Mismatches 29; Indels 1; Gaps 1;

QY 1 MRGATRVISMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGRGECH 60
Db 1 MKCFAIVVLLLVIAFHSHGAVITGACDKDVQCGSGTCCCAASAWSNRIRFCIPLNGSGEDC 60

QY 61 HPGSHKVPFFRKRKHHTCPCLPNLLCSRPDPGRYRC 97
Db 61 HPASHKVPYDGRKRLSLCPCSKGLTCKSGE-KFKCS 96

RESULT 11
PRK2_HUMAN STANDARD; PRT; 129 AA.
AC Q9HC23;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Prokineticin 2 precursor (PK2) (Protein Bv8 homolog).
DE Name=PROK2; Synonyms=BV8;
GN
```

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE OF 5-129 FROM N.A. (ISOFORM 1).
 RC TISSUE=Testis;
 RX MEDLINE=20047850; PubMed=10580115; DOI=10.1016/S0014-5793(99)01473-8;
 RA Wechsberger C., Puglisi R., Lepperdinger G., Boitani C., Kreil G.;
 RT "The mammalian homologue of Bv8 from frog skin is mainly expressed in
 spermatocytes.";
 RL FEBS Lett. 462:177-181(1999).
 [2]
 RN SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=21160229; PubMed=11259612;
 RA Li M., Bullock C.M., Knauer D.J., Ehler F.J., Zhou Q.-Y.;
 RT "Signal peptide prediction based on analysis of experimentally
 verified cleavage sites.";
 RL Protein Sci. 13:2819-2824(2004).
 CC -!- FUNCTION: May function as an output molecule from the
 CC suprachiasmatic nucleus (SCN) that transmits behavioral circadian
 CC rhythm. May also function locally within the SCN to synchronize
 CC output. Potentially contracts gastrointestinal (GI) smooth muscle.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms-2;
 CC Name=1;
 CC IsoId=Q9HC23-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9HC23-2; Sequence=VSP 005219;
 CC TISSUE SPECIFICITY: Expressed in the testis and, at low levels, in
 CC the small intestine.
 CC -!- INDUCTION: Activated by CLOCK and BMAL1 heterodimers and light;
 CC inhibited by period genes (PER1, PER2 and PER3) and cryptochrome
 CC genes (CRY1 and CRY2) (Probable).
 CC -!- SIMILARITY: Belongs to the prokinectin family.
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 CC -----
 DR EMBL; AF182069; AAG16893.2; -;
 DR EMBL; AF333025; AAK49919.1; -;
 DR HSSP; P25687; 1IMT.
 DR Genew; HGNC:18455; PROK2.
 DR MIM; 607002; -;
 DR GO; GO:0005576; C:extracellular; TAS.
 DR GO; GO:0001664; F:G-protein-coupled receptor binding; TAS.
 DR GO; GO:0000187; P:activation of MAPK; TAS.
 DR GO; GO:0001525; P:angiogenesis; IDA.
 DR GO; GO:0006916; P:anti-apoptosis; IDA.
 DR GO; GO:0008283; P:cell proliferation; IDA.
 DR GO; GO:0006935; P:chemotaxis; IDA.
 DR GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; NAS.
 DR GO; GO:0006954; P:inflammatory response; NAS.
 DR GO; GO:0019233; P:perception of pain; TAS.
 DR GO; GO:0045987; P:positive regulation of smooth muscle contra. .; IDA.
 DR GO; GO:0007283; P:spermatogenesis; IMP.
 DR InterPro; IPR009523; Prokinectin.
 DR Pfam; PF06607; Prokinectin; 1.
 KW Alternative splicing; Biological rhythms; Direct protein sequencing;

KW Neuropeptide; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 129
 FT DISULFID 34 46
 FT DISULFID 40 58
 FT DISULFID 45 107
 FT DISULFID 68 115
 FT DISULFID 109 125
 FT VARSPLIC 75 95
 FT Missing (in isoform 2).
 FT /FTId=VSP_005219.
 SQ SEQUENCE 129 AA; 14314 MW; 0487679E8700DA55 CRC64;
 Query Match 48.0%; Score 282.5; DB 1; Length 129;
 Best Local Similarity 44.4%; Pred. No. 5e-21;
 Matches 48; Conservative 15; Mismatches 24; Indels 21; Gaps 1;
 QY 10 MLLLVTVSDCAVITGACERDVQCGAGTCATSLMLRGLRMCTPLGRGEECHPGSHK--- 66
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 18 LLLTPRAGDAAVITGACDKSQCGGMCACVSIWVKISIRICTPMGKLGDSCHPLTRKNF 77
 QY 67 -----VPEFRKRKHHTCPCPLNLLCSRFPDGYRC 96
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 78 GNGRQERRKRKRKRKKEVPFFGRMHHTCPCPLGCLARTSFNRFC 125
 RESULT 12
 PRK2_MOUSE
 ID PRK2_MOUSE STANDARD; PRT; 128 AA.
 AC Q9QXU7; Q9QXU5; Q9QXU6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Prokinectin 2 precursor (PK2) (Protein Bv8 homolog).
 GN Name=Prok2; Synonyms=Bv8;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX STRAIN=129/SV;
 RC MEDLINE=20047850; PubMed=10580115; DOI=10.1016/S0014-5793(99)01473-8;
 RA Wechsberger C., Puglisi R., Lepperdinger G., Boitani C., Kreil G.;
 RT "The mammalian homologue of Bv8 from frog skin is mainly expressed in
 RT spermatocytes.";
 RL FEBS Lett. 462:177-181(1999).
 [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RC STRAIN=129/SV;
 RX PubMed=11054548; DOI=10.1016/S0378-1119(00)00355-3;
 RA Jilek A., Engel E., Beier D., Lepperdinger G.;
 RT "Murine Bv8 gene maps near a syntenic breakpoint of mouse chromosome 6
 RT and human 3p21.";
 RL Gene 256:189-195(2000).
 [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2), AND FUNCTION.
 RC STRAIN=C57BL/6;
 RX MEDLINE=22022134; PubMed=12024206; DOI=10.1038/417405a;
 RA Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J.,
 RA Weaver D.R., Leslie F.M., Zhou Q.-Y.;
 RT "Prokinectin 2 transmits the behavioural circadian rhythm of the
 RT suprachiasmatic nucleus.";
 RL Nature 417:405-410(2002).
 [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,


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QY 67 -----VPPFRKKHHTCPCLPNLLCSRPDPGRYRC 96
Db 77 ANGRQERRAKRKRKKEVFFWGRMHHTCPCLPLGLACLRISFNRFIC 124

RESULT 14
Q8JFE6 PRELIMINARY; PRT; 96 AA.
AC Q8JFE6;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DE 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Bm8-a protein precursor (Bv8 protein homolog 1).
OS Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=161274;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Chen T., Farragher S., Bjourson A.J., Orr D.P., Rao P., Shaw C.;
RT "Granular gland secretions in stimulated amphibian skin
secretions.";
RL J. Biochem. 371:125-130(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin secretions;
RX MEDLINE=22515712; PubMed=12628381; DOI=10.1016/S1096-4959(02)00294-4;
RA Lai R., Liu H., Lee W.H., Zhang Y.;
RT "Two novel Bv8-like peptides from skin secretions of the toad Bombina
maxima.";
RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 134:509-514(2003).
DR EMBL; AJ440230; CAD293340.1; -.
DR EMBL; AF411090; AAN03821.1; -.
DR HSSP; P25687; 1IMT.
DR InterPro; IPR009523; Prokineticin.
DR Pfam; PF06607; Prokineticin; 1.
KW SIGNAL.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 96 Bm8-a protein.
SQ SEQUENCE 96 AA; 10117 MW; 2269AAC8654B18A6 CRC64;

Query Match 46.6%; Score 274.5; DB 2; Length 96;
Best Local Similarity 49.5%; Pred. No. 2.4e-20;
Matches 48; Conservative 17; Mismatches 31; Indels 1; Gaps 1;

QY 1 MRGATRVSIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGEC 60
Db 1 MKCFAQIVVLLLVIAFSGHGVITGCDRDAQCGSGTCCCAAGAFSRNIRFCVPLGNNGEC 60

QY 61 HPGSHKVPFFPKRKHHTCPCLPNLLCSRPDPGRYRC 97
Db 61 HPASHKVPYNGKRLSSLCPCNTGLTCSKSGE-KFQCS 96

Query Match 46.6%; Score 274.5; DB 2; Length 96;
Best Local Similarity 49.5%; Pred. No. 2.4e-20;
Matches 48; Conservative 17; Mismatches 31; Indels 1; Gaps 1;

QY 1 MRGATRVSIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGEC 60
Db 1 MKCFAQIVVLLLVIAFSGHGVITGCDRDAQCGSGTCCCAAGAFSRNIRFCVPLGNNGEC 60

QY 61 HPGSHKVPFFPKRKHHTCPCLPNLLCSRPDPGRYRC 97
Db 61 HPASHKVPYNGKRLSSLCPCNTGLTCSKSGE-KFQCS 96

RESULT 15
Q8JFX8 PRELIMINARY; PRT; 96 AA.
AC Q8JFX8;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DE 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Bm8-f protein precursor
OS Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=161274;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Chen T., Farragher S., Bjourson A.J., Orr D.P., Rao P., Shaw C.;
RT "Granular gland secretions in stimulated amphibian skin
secretions.";
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RL J. Biochem. 371:125-130(2003).
DR EMBL; AJ440235; CAD29345.1; -.
DR HSSP; P25687; 1IMT.
DR InterPro; IPR009523; Prokineticin.
DR Pfam; PF06607; Prokineticin; 1.
KW SIGNAL.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 96 Bm8-f protein.
SQ SEQUENCE 96 AA; 10058 MW; 2269A070FFE118A6 CRC64;

Query Match 46.4%; Score 273.5; DB 2; Length 96;
Best Local Similarity 50.5%; Pred. No. 3.1e-20;
Matches 49; Conservative 15; Mismatches 32; Indels 1; Gaps 1;

QY 1 MRGATRVSIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGEC 60
Db 1 MKCFAQIVVLLLVIAFSGHGVITGCDRDAQCGSGTCCCAAGAFSRNIRFCVPLGNNGEC 60

QY 61 HPGSHKVPFFPKRKHHTCPCLPNLLCSRPDPGRYRC 97
Db 61 HPASHKVPDSGKRLSSLCPCNTGLTCSKSGE-KYQCS 96

Search completed: November 1, 2005, 14:52:00
Job time : 179 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 14:43:20 ; Search time 42 Seconds
(without alignments)
186.623 Million cell updates/sec

Title: US-10-027-603-2
Perfect score: 589
Sequence: 1 MRGATRVSLMLLLVTVSDCA.....CSRFPDGRYRCMDLKNINF 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	589	100.0	105	US-10-212-201A-5	Sequence 5, Appli
3	589	100.0	105	US-10-212-355-5	Sequence 5, Appli
4	577	98.0	105	US-09-621-976-5350	Sequence 5350, Ap
5	448	76.1	80	US-09-513-999C-4698	Sequence 4698, Ap
6	303	51.4	108	US-09-712-529-2	Sequence 2, Appli
7	303	51.4	108	US-10-212-201A-2	Sequence 2, Appli
8	303	51.4	108	US-10-212-355-2	Sequence 2, Appli
9	107.5	18.3	224	US-09-161-241-14	Sequence 14, Appl
10	102	17.3	186	US-09-949-016-7146	Sequence 146, Ap
11	102	17.3	207	US-09-161-241-13	Sequence 13, Appl
12	102	17.3	259	US-09-161-241-12	Sequence 12, Appl
13	102	17.3	259	US-09-949-016-6872	Sequence 6872, Ap
14	101	17.1	259	US-09-161-241-11	Sequence 11, Appl
15	100.5	17.1	350	US-09-161-241-9	Sequence 9, Appli
16	100.5	17.1	350	US-09-907-794A-236	Sequence 236, App
17	100.5	17.1	350	US-09-905-125A-236	Sequence 236, App
18	100.5	17.1	350	US-09-902-775A-236	Sequence 236, App
19	100.5	17.1	350	US-09-906-700-236	Sequence 236, App
20	100.5	17.1	350	US-09-903-603A-236	Sequence 236, App
21	100.5	17.1	350	US-09-904-920A-236	Sequence 236, App
22	100.5	17.1	350	US-09-909-064-236	Sequence 236, App
23	100.5	17.1	350	US-09-905-381A-236	Sequence 236, App
24	100.5	17.1	350	US-09-906-618-236	Sequence 236, App
25	100.5	17.1	375	US-09-949-016-7856	Sequence 7856, Ap
26	100.5	17.1	375	US-09-949-016-7857	Sequence 7857, Ap
27	100.5	17.1	375	US-09-949-016-7858	Sequence 7858, Ap

28	98.5	16.7	349	3	US-09-161-241-8	Sequence 8, Appli
29	97	16.5	266	3	US-09-161-241-10	Sequence 10, Appl
30	97	16.5	266	4	US-09-976-594-1086	Sequence 1086, Ap
31	82	13.9	1342	4	US-09-561-709B-13	Sequence 13, Appl
32	81	13.8	1964	3	US-09-467-997-1	Sequence 1, Appli
33	79	13.4	124	4	US-09-949-016-11293	Sequence 11293, A
34	78.5	13.3	163	2	US-08-219-237B-5	Sequence 5, Appli
35	78.5	13.3	163	3	US-08-477-347-13	Sequence 13, Appl
36	78.5	13.3	163	3	US-08-476-862-4	Sequence 4, Appli
37	78.5	13.3	163	3	US-08-468-560C-5	Sequence 5, Appli
38	78.5	13.3	163	4	US-09-800-909-4	Sequence 4, Appli
39	78.5	13.3	163	4	US-09-800-908-13	Sequence 13, Appl
40	75.5	12.8	1101	4	US-09-561-709B-5	Sequence 5, Appli
41	75.5	12.8	1761	4	US-09-561-709B-1	Sequence 1, Appli
42	75	12.7	546	4	US-09-949-016-10394	Sequence 10394, A
43	75	12.7	651	1	US-08-264-101-2	Sequence 2, Appli
44	75	12.7	651	2	US-08-765-243-2	Sequence 2, Appli
45	75	12.7	651	5	PCT-US95-07295-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-712-529-5
; Sequence 5, Application US/09712529
; Patent No. 6485938
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/09/712,529
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-712-529-5

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Best Local Similarity	100.0%;	Pred. No. 9.3e-59;		
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Db	1	MRGATRVSLMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRMCTPLGREGEC	60	
QY	61	HPGSHKVPFFRRKHHTCTCPLNLLCSRPDPGRYRCMDLKNINF	105	
Db	61	HPGSHKVPFFRRKHHTCTCPLNLLCSRPDPGRYRCMDLKNINF	105	

RESULT 2
US-10-212-201A-5
; Sequence 5, Application US/10212201A
; Patent No. 6756479
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Whitmore, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/10/212,201A
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US/09/712,529
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 7

polyptide primary data of applicant

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-201A-5

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	Best Local Similarity	100.0%	Pred. No. 9.3e-59		
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Db	1	MRGATRVSIIMLLLVTSDCAVITGACERDVOCGAGTCCATSLWLRGLRMCTPLRGREGBEC	60		
Qy	61	HPGSHKVPFFFRKRHHHTCPCLPNLLCSRFDPGRYRCSDMLKNINF	105		
Db	61	HPGSHKVPFFFRKRHHHTCPCLPNLLCSRFDPGRYRCSDMLKNINF	105		

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RESULT 3
US-10-212-355-5
  Sequence 5, Application US/10212355
  Patent No. 6828425
  GENERAL INFORMATION:
  APPLICANT: Sheppard, Paul O.
  APPLICANT: Bishop, Paul D.
  APPLICANT: Whitmore, Theodore E.
  APPLICANT: Thompson, Penny P.
  TITLE OF INVENTION: Human Zven Protein
  FILE REFERENCE: 99-81
  CURRENT APPLICATION NUMBER: US/10/10-212-355-5
  CURRENT FILING DATE: 2002-08-02
  NUMBER OF SEQ ID NOS: 7
  SOFTWARE: FastSeq for Windows Vers 1.0
  SEQ ID NO 5
  LENGTH: 105
  TYPE: PRT
  ORGANISM: Homo sapiens
US-10-212-355-5

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	Best Local Similarity	100.0%	Pred. No. 9.3e-59		
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RESULT 4
US-09-621-976-5350
; Sequence 5350, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5350
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

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; NAME/KEY: SIGNAL
; LOCATION: -19..-1
; NAME/KEY: UNSURE
; LOCATION: 38
; OTHER INFORMATION: Xaa = Ala,Gly
US-09-621-976-5350

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RESULT 5
US-09-513-999C-4698
; Sequence 4698, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4698
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -19..-1
; OTHER INFORMATION: score 7.2
; OTHER INFORMATION: seq VSIMLLVTVSDC/AV
US-09-513-999C-4698

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Best Local Similarity 98.8%; Pred No. 4.7e-43;
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Db    1 MRGATRVSMILLVTVSDCAVTTCGERDVQCAGTCCCAISLWRLGRMCTPLGRGGEEC 60

Qy   61 HPGSHKVPPFRKRKHHITPCP 80
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Db    61 HPGSHKIPIPRKRKHHTCP 80
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RESULT 6
US-09-712-529-2
; Sequence 2, Application US/09712529
; Patent NO. 6485938
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/09/712-529

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; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-712-529-2

Query Match      51.4%; Score 303; DB 4; Length 108;
Best Local Similarity 55.2%; Pred. No. 1.2e-26;
Matches 48; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 10 MLLLVTSQCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGECHPGSHKVPF 69
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Db 18 LLTTPRAGDAAVITGACDXDSCGGGMCACAVSIWKSIRICTPMGKLGDSCHPLTRKVPF 77
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QY 70 FRKRKHHTCPCLPNLLCSRFPDGRYRC 96
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 78 FGRMHHTCPCLPGLACLRSTFNRFC 104
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7
US-10-212-201A-2
; Sequence 2, Application US/10212201A
; Patent No. 6756479
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/10/212,201A
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US/09/712,529
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-201A-2

Query Match      51.4%; Score 303; DB 4; Length 108;
Best Local Similarity 55.2%; Pred. No. 1.2e-26;
Matches 48; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 10 MLLLVTSQCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGECHPGSHKVPF 69
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Db 18 LLTTPRAGDAAVITGACDXDSCGGGMCACAVSIWKSIRICTPMGKLGDSCHPLTRKVPF 77
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QY 70 FRKRKHHTCPCLPNLLCSRFPDGRYRC 96
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Db 78 FGRMHHTCPCLPGLACLRSTFNRFC 104
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RESULT 8
US-10-212-355-2
; Sequence 2, Application US/10212355
; Patent No. 6828425
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/10/212,355
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 2
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-355-2

Query Match      51.4%; Score 303; DB 4; Length 108;
Best Local Similarity 55.2%; Pred. No. 1.2e-26;
Matches 48; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 10 MLLLVTSQCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGECHPGSHKVPF 69
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Db 18 LLTTPRAGDAAVITGACDXDSCGGGMCACAVSIWKSIRICTPMGKLGDSCHPLTRKVPF 77
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QY 70 FRKRKHHTCPCLPNLLCSRFPDGRYRC 96
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Db 78 FGRMHHTCPCLPGLACLRSTFNRFC 104
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RESULT 9
US-09-161-241-14
; Sequence 14, Application US/09161241
; Patent No. 6344541
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B
; APPLICANT: Sullivan, John K
; APPLICANT: Theill, Lars E
; APPLICANT: Wang, Daguang
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
; FILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/161,241
; CURRENT FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Human
US-09-161-241-14

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Best Local Similarity 35.5%; Pred. No. 0.00025;
Matches 22; Conservative 5; Mismatches 32; Indels 3; Gaps 1;

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QY 85 LC 86
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Db 201 LC 202
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RESULT 10
US-09-949-016-7146
; Sequence 7146, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7146
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Best Local Similarity 31.5%; Pred. No. 0.0016;
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Db 235 KGLSCKVWKDATY 247

RESULT 15
US-09-161-241-9
; Sequence 9, Application US/09161241
; Patent No. 6344541
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B
; APPLICANT: Sullivan, John K
; APPLICANT: Theill, Lars E
; APPLICANT: Wang, Daquang
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
; FILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/161,241
; CURRENT FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Human
US-09-161-241-9

Query Match 17.1%; Score 100.5; DB 3; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.0025;
Matches 26; Conservative 3; Mismatches 29; Indels 11; Gaps 4;
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Db 208 CDNRDCQFGLCAFAQ---RGLLPVCTPLPVEGELCHDPASRLDLITWELEPDGALDR 264
QY 78 CPCLPNLLC 86
Db 265 CPCASGLLC 273

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

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(without alignments)
201.821 Million cell updates/sec

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Minimum DB seq length: 0
Maximum DB seq length: 86

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	54	10.8	63	2 S08572	chymotrypsin/elast
5	53.5	10.7	57	2 A46654	growth modulatory
6	53	10.6	47	2 B58319	gamma-zeathionin 2
7	53	10.6	77	2 S29563	endothelin 2 precu
8	52.5	10.5	70	2 A55824	drosomycin precurs
9	52	10.4	77	2 S47158	metallothionein II
10	51.5	10.3	77	2 AF2564	hypothetical prote
11	51	10.2	84	2 JN0469	85K MRK-20 recogni
12	50.5	10.1	47	2 S69145	gamma-thionin SI-a
13	49.5	9.9	61	2 C81079	hypothetical prote
14	49.5	9.9	74	2 S05594	pseudochionin St1
15	49	9.8	62	2 I51538	metallothionein -
16	49	9.8	65	2 S03858	carboxypeptidase A
17	49	9.8	67	2 FC4008	hypothetical prote
18	49	9.8	72	2 A42325	orf 5' to pheC - p
19	48.5	9.7	54	1 S23075	protein PMP-D1 - m
20	48.5	9.7	79	2 T06381	proteinase inhibit
21	48	9.6	66	2 S59621	metallothionein is
22	48	9.6	67	2 B69830	hypothetical prote
23	48	9.6	74	2 AF3436	hypothetical prote
24	47.5	9.5	64	2 A25775	metallothionein A
25	47.5	9.5	65	1 NTSR3C	neurotoxin 3 - bar
26	46.5	9.3	58	2 AD0841	hypothetical prote
27	46.5	9.3	65	1 NTSR1C	neurotoxin 1 - bar
28	46	9.2	43	2 JC2554	holotricin 1 - Hol
29	46	9.2	44	2 I48942	cellular disintegr

RESULT 1

T26545
hypothetical protein YIA5A.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26545
R:Barlow, K.
submitted to the EMBL Data Library, January 1998
A:Reference number: Z20228
A:Accession: T26545
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-83 <WIL>
A:Cross-references: UNIPROT:Q9XXT6; EMBL:AL021177; PIDN:CAAL5979.1; GSPDB:GN00021; CESP
A:Experimental source: clone YIA5A
C:Genetics:
A:Gene: CESP:YIA5A.2
A:Map position: 3
A:Introns: 27/2

Query Match 12.3%; Score 61.5; DB 2; Length 83;
Best Local Similarity 37.5%; Pred. No.13;
Matches 18; Conservative 1; Mismatches 10; Indels 19; Gaps 3;

QY 17 TCCATSLWLRGLRMCTPLGREGECHP-GSHKVPFRKXKHTCPCLP 63
DB 48 TCCCSISL-----GASAHPTRSRPVP----RKQHTAPSPPP 77

RESULT 2

A44794
antimicrobial peptide eNAP-1 - horse (fragment)
C:Species: Equus caballus (domestic horse)
C>Date: 24-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A44794; A40833
R:Couto, M.A.; Harwig, S.S.; Cullor, J.S.; Hughes, J.P.; Lehrer, R.I.
Infect. Immun. 60, 3065-3071, 1992
A>Title: Identification of eNAP-1, an antimicrobial peptide from equine neutrophils.
A:Reference number: A44794; MUID:92347972; PMID:1639474
A:Accession: A44794
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-46 <COU>
A:Cross-references: UNIPROT:P80930
A:Experimental source: neutrophils
A>Note: sequence extracted from NCBI backbone (NCBI:P109730)
C:Superfamily: granulins

Query Match 11.6%; Score 58; DB 2; Length 46;
Best Local Similarity 33.3%; Pred. No.18;
Matches 17; Conservative 3; Mismatches 23; Indels 8; Gaps 2;

[illegible]

A;Experimental source: seeds
A;Note: this is a revision to the sequence from reference S13931
R;Bloch Jr., C.; Richardson, M.
FBS Lett. 279, 101-104, 1991
A;Title: A new family of small (5 kDa) protein inhibitors of insect alpha-amylases from
A;Reference number: S13931; MUID:91138737; PMID:1995329
A;Accession: S13931
A;Molecule type: protein
A;Residues: 1-4, 'GK', 7-34, 'R', 36-47 <BLO>
A;Experimental source: seeds
A;Note: this sequence has been revised in reference S69144
C;Superfamily: gamma-thionin
C;Keywords: alpha-amylase inhibitor
F;3-47,14-36,20-41,24-43/disulfide bonds: #status experimental

Query Match 10.1%; Score 50.5; DB 2; Length 47;
Best Local Similarity 35.7%; Pred. No. 1.1e+02;
Matches 10; Conservative 4; Mismatches 5; Indels 9; Gaps 1;

QY 41 CHPGSHKVPFFRKRRKHTCPCLPNLLCS 68
| | | | | : | | : | | | |
Db 3 CMKGS-----OHHSPFCISDLCS 21

RESULT 13
C81079
hypothetical protein NMB1477 [imported] - Neisseria meningitidis (strain MC58 serogroup
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: C81079
R;Tetzelin, H.; Saunders, N.J.; Heidekamp, F.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzbach, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizzi, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: C81079
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-61 <TET>
A;Cross-references: UNIPROT:Q9JYQ4; GB:AE002497; GB:AE002098; NID:g7226712; PIDN:AAF4183
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB1477

Query Match 9.9%; Score 49.5; DB 2; Length 61;
Best Local Similarity 28.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 4; Mismatches 26; Indels 11; Gaps 3;

QY 9 RDVQCGAGTCCALSL-----WLRLMCTPLGREGECHPGS--HKVPFFRKRRKH 57
| | | | | : | | : | | | |
Db 7 RRIQGLGNKIIRLIKSGRFQLHAITFLKI---GYSCPDGLFHSFLFVKKQN 60

RESULT 14
S05594
pseudothionin St1 precursor - potato (strain cv. Bintje)
C;Species: Solanum tuberosum (potato)
A;Variety: strain cv. Bintje
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S05594; S45659
R;Stiekema, W.J.; Heidekamp, F.; Dirkse, W.G.; van Beckum, J.; de Haan, P.; ten Bosch, C.
Plant Mol. Biol. 11, 255-269, 1988
A;Title: Molecular cloning and analysis of four potato tuber mRNAs.
A;Reference number: S05592
A;Accession: S05594
A;Molecule type: mRNA
A;Residues: 1-74 <ST1>
A;Cross-references: UNIPROT:P20346; EMBL:X13180; NID:g21393; PIDN:CAA31577.1; PID:g21394
A;Experimental source: strain cv. Bintje
A;Note: it is unknown whether 1-Met is the initiator or whether translation is initiated
A;Note: the authors designated this protein as proteinase inhibitor (Bowman Birk) homolod

R;Moreno, M.; Segura, A.; Garcia-Olmedo, F.
Eur. J. Biochem. 223, 135-139, 1994
A;Title: Pseudothionin-St1, a potato peptide active against potato pathogens.
A;Reference number: S45659; MUID:94307252; PMID:8033886
A;Accession: S45659
A;Molecule type: protein
A;Residues: 28, 'N', 30-47 <MOR>
A;Experimental source: strain cv. Desiree
C;Superfamily: gamma-thionin
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-74/Product: pseudothionin St1 #status experimental <MAT>

Query Match 9.9%; Score 49.5; DB 2; Length 74;
Best Local Similarity 26.3%; Pred. No. 2.1e+02;
Matches 15; Conservative 3; Mismatches 18; Indels 21; Gaps 2;

QY 5 GACRDVQCGAGTCCALSLWLRLMCTPLGREGECHPGSHKVPFFRKRRKHTCPC 61
| | | | | : | | : | | | |
Db 39 GPCTRDSNCAS-----VCETERFSGNCHG-----FRRRCFCTKPC 74

RESULT 15
I51538
metallothionein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I51538
R;Saint-Jacques, E.; Seguin, C.
DNA Cell Biol. 12, 329-340, 1993
A;Title: Cloning and nucleotide sequence of a complementary DNA encoding Xenopus laevis
A;Reference number: I51538; MUID:93263990; PMID:8494609
A;Accession: I51538
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-62 <SAI>
A;Cross-references: UNIPROT:Q05890; GB:M96729; NID:g214585; PIDN:AB559949.1; PID:g214586
C;Superfamily: metallothionein

Query Match 9.8%; Score 49; DB 2; Length 62;
Best Local Similarity 26.7%; Pred. No. 2e+02;
Matches 16; Conservative 4; Mismatches 28; Indels 12; Gaps 3;

QY 7 CERDVQCGAGTCCALSL-----LWLRLMCTPLGREGECHPGSHKVPFFRKRRKHTCPC 61
| | | | | : | | : | | | |
Db 8 CETGASCSCGTCTCSNCKTSCKSCCCP--AECSKCSQGCHCEKSKK-----CSC 60

Search completed: November 1, 2005, 15:13:04
Job time : 42 secs

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OM protein - protein search, using sw model

Run on: November 1, 2005, 14:53:41 ; Search time 173 Seconds
(without alignments)
254.560 Million cell updates/sec

Title: US-10-027-603-2_COPY_20_105
Perfect score: 498
Sequence: 1 AVITGACRDRVQCGAGTCCA.....CSRFPDGRYRCMDLKNINF 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 188592

Minimum DB seq length: 0
Maximum DB seq length: 86

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_spot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	432	86.7	81	2 Q8K457	Q8K457 mus musculus
2	310.5	62.3	81	1 VPRA_DENPO	P25687 dendroaspis
3	73	14.7	64	1 TX16_PHORI	P83893 phoneutria
4	70	14.1	68	1 TX16_PHONI	P83997 phoneutria
5	66	13.3	85	1 HEPC_MORCS	P82951 morone chry
6	63.5	12.8	70	1 CX2X_CONBE	Q93233 conus betul
7	61.5	12.3	83	2 Q9XXT6	Q93233 caenorhabdi
8	58.5	11.7	76	2 Q64DV8	Q64dv8 uncultured
9	58.5	11.7	76	2 Q64AE9	Q64ae9 uncultured
10	58	11.6	46	1 ENA1_HORSE	P80930 equus caball
11	57.5	11.5	68	1 ACTX_HADVE	P81803 hadronyche
12	56	11.2	78	1 MT2_MUSAC	O22319 musa acumin
13	55.5	11.1	57	2 Q9PRN7	Q9prn7 carassius a
14	55.5	11.1	76	2 Q7UUQ0	Q7uuq0 rhodopiirell
15	55.5	11.1	80	2 Q9GS92	Q9gs92 homo sapien
16	55	11.0	49	2 Q8H6K2	Q8b6k2 brassica ra
17	54.5	10.9	57	1 GRN3_CYPCA	P81015 cyprinus ca
18	54.5	10.9	78	1 LCK3_ARATH	P82718 arabidopsis
19	54	10.8	72	2 Q8TB48	Q8tb48 homo sapien
20	54	10.8	75	1 LC20_ARATH	P82734 arabidopsis
21	54	10.8	75	2 Q8K4W3	Q8k4w3 mus musculus
22	53.5	10.7	57	1 GRN1_CYPCA	P81013 cyprinus ca
23	53.5	10.7	60	1 MTH_CTPS1	Q92044 cyprinodon
24	53.5	10.7	60	2 Q71DA0	Q71da0 drosophila
25	53.5	10.7	63	2 Q7QRL9	Q7qrl9 giardia lam
26	53	10.6	47	1 SIA1_SORBI	P21923 sorghum bic
27	53	10.6	47	1 TH22_WAIZE	P81009 zea mays (m
28	53	10.6	67	2 Q7NG77	Q7ng77 gloebacter
29	52.5	10.5	68	1 MT_LYTPI	O02033 lytechinus
30	52.5	10.5	70	1 DMVC_DROME	P41964 drosophila
31	52.5	10.5	75	1 LCR6_ARATH	P82721 arabidopsis

32	52.5	10.5	86	2 Q74N55	Q74n55 nanoarchaeu
33	52	10.4	60	2 Q8MSH6	Q8msh6 drosophila
34	52	10.4	65	1 ICE2_ASCSU	P07852 ascaris suu
35	52	10.4	76	1 EC_MAIZE	P43401 zea mays (m
36	52	10.4	84	1 SCX9_CENSC	Q95wc9 centruridae
37	51.5	10.3	48	2 Q8RUW5	Q6ruw5 carassius c
38	51.5	10.3	59	1 R323_ENTFA	Q83rd enterococcu
39	51.5	10.3	67	2 Q96717	Q96717 fucus vesic
40	51.5	10.3	74	2 Q8WQ95	Q8wq95 crassostrea
41	51.5	10.3	77	2 Q75WH3	Q75wh3 macrothele
42	51.5	10.3	77	2 Q8YK17	Q8yk17 anabaena sp
43	51.5	10.3	78	2 Q8WB66	Q8wb66 nicotiana t
44	51.5	10.3	85	2 Q8FA94	Q8fa94 escherichia
45	51	10.2	73	2 Q86RB8	Q86rb8 trypanosoma

ALIGNMENTS

```
RESULT 1
Q8K457 PRELIMINARY; PRT; 81 AA.
AC Q8K457;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Prokineticin 1 (Fragment).
GN Name=Prok1; Synonyms=Pkl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=2022134; PubMed=12024206; DOI=10.1038/417405a;
RA Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bernak J.C., Belluzzi J.,
RT Weaver D.R., Leslie F.M., Zhou Q.Y.;
RT "Prokineticin 2 transmits the behavioural circadian rhythm of the
suprachiasmatic nucleus.";
RL Nature 417:405-410(2002).
DR EMBL; AF487281; AAM49573.1; -.
DR HSSP; P25687; 1IMT.
DR MGD; MGI:2180370; Prok1.
DR GO; GO:005576; C:extracellular; IDA.
DR GO; GO:0000187; P:activation of MAPK; IDA.
DR GO; GO:0007623; P:circadian rhythm; TAS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR GO; GO:0045765; P:regulation of angiogenesis; IDA.
DR InterPro; IPR009523; Prokineticin.
DR Pfam; PF06607; Prokineticin; 1.
FT NON_TER
SQ SEQUENCE 81 AA, 9192 MW, 78BE3EC6B16A8011 CRC64;
Query Match 86.7%; Score 432; DB 2; Length 81;
Best Local Similarity 87.7%; Pred. No. 3.5e-38;
Matches 71; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
Qy 6 ACERDVOCAGTCCCAISLWGLRMLCTPLGREGECCHPGSHKVPFRKREKHTTCPLNPL 65
Db 1 ACERDIQCGAGTCCCAISLWGLRLCTPLGREGECCHPGSHKIPFLRKQKHHTCPCPSL 60
Qy 66 LCSRPDPGRYRCMDLKNINF 86
Db 61 LCSRPDPGRYRCFRDLKNANF 81
RESULT 2
VPRA_DENPO STANDARD; PRT; 81 AA.
ID VPRA_DENPO
AC P25687;
DT 01-MAY-1992 (Rel. 22, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
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25-OCT-2004 (Rel. 45, Last annotation update)
DE Intestinal toxin 1 (MIT 1) (MIT1) (Venom protein A).
OS Dendroaspis polylepsis polylepsis (Black mamba).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scieroglossa; Serpentes; Colubroidea;
OC Elapidae; Elapinae; Dendroaspis.
OX NCBI TaxID=8620;
RN [1]_
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=81115818; PubMed=7461607;
RA Joubert F.J., Strydom D.J.;
RT "Snake venom. The amino acid sequence of protein A from Dendroaspis
RT polylepsis polylepsis (black mamba) venom.";
RL Hoppe-Seyler's Z. Physiol. Chem. 361:1787-1794 (1980).
RN [2]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=20036442; PubMed=10567694; DOI=10.1016/S0014-5793(99)01459-3;
RA Schweitz H., Pascaud P., Diocot S., Moinier D., Lazdunski M.;
RT "MIT1, a black mamba toxin with a new and highly potent activity on
RT intestinal contraction.";
RL FEBS Lett. 461:183-188 (1998).
RN [3]
RP STRUCTURE BY NMR.
RC TISSUE=Venom;
RX MEDLINE=98437381; PubMed=9761684; DOI=10.1006/jmbi.1998.2057;
RA Boisbouvier J., Albrand J.-P., Blackledge M., Jaquinod M.,
RA Schweitz H., Lazdunski M., Marion D.;
RT "A structural homologue of colipase in black mamba venom revealed by
RT NMR floating disulphide bridge analysis.";
RL J. Mol. Biol. 283:205-219 (1998).
CC -!- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the prokinectin family.
DR PDB; 1LMT; NMR; @=1-81.
DR InterPro; IPR009523; Prokinectin.
DR Pfam; PF06607; Prokinectin; 1.
KW 3D-structure; Direct protein sequencing; Toxin.
FT DISULFID 7 19
FT DISULFID 13 31
FT DISULFID 18 60
FT DISULFID 41 68
FT DISULFID 62 73
FT DISULFID 73 78
FT VARIANT 73 78 P -> Q (in protein A').
FT CONFLICT 18 18 C -> S (in Ref. 1).
FT CONFLICT 22 22 S -> C (in Ref. 1).
SQ SEQUENCE 81 AA; 8645 MW; 6C01368841572044 CRC64;

Query Match 62.3%; Score 310.5; DB 1; Length 81;
Best Local Similarity 62.8%; Pred. No. 2.4e-25;
Matches 49; Conservative 14; Mismatches 14; Indels 1; Gaps 1;

QY 1 AVITGACERDVQCGAGTCCALISLWRLGRLMCTPLGREGECHPGSHKVPFFRKHK-HHTC 59
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
1 AVITGACERDLQCGKGTCCAVSLWIKSVRVCTPVGTSGEDCHPASHKIPFSGQRWHTC 60
QY 60 PCLNLLCSRFPDGRYRC 77
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
61 PCAPNLACVQTSPPKFKC 78

RESULT 3
TX16_PHONI
ID TX16_PHONI STANDARD; PRT; 64 AA.
AC P83893;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Non-toxic venom protein PRTx16C0.
OS Phoneutria reidyi (Brazilian Amazonian armed spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.
OX NCBI TaxID=272752;

Query Match 14.1%; Score 70; DB 1; Length 68;
Best Local Similarity 27.5%; Pred. No. 5.3;
Matches 19; Conservative 6; Mismatches 28; Indels 16; Gaps 3;

QY 3 ITGACERDVQCGAGTCCALISLWRLGRLMCTPLGREGECHPGSHKVPFFRKHKHT- 58
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
3 IPGQSCINADCGEGCCTGGSY---NRHCQSLADGTPCQKENDYNEVKF-----GCPCKEGL 50
QY 59 CPCLPNLLC 67
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
51 CPCKEGLMC 59

[1]
RN SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS
RP SPECTROMETRY.
RC TISSUE=Venom;
RA Richardson M., Pimenta A.M.C., Benquerer M.P., Santoro M.M.,
RA Figueiredo S.G., Cordeiro M.N.;
RT "Non-toxic protein PRTx16C0 from venom of Brazilian Amazonian armed
RT spider Phoneutria reidyi has sequence similarities with toxins from
RT other spiders.";
RL Submitted (MAY-2004) to Swiss-Prot.
CC -!- FUNCTION: Non-toxic to mice and insects.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- MASS SPECTROMETRY: MW=6981.39; METHOD=Electrospray; RANGE=1-64;
CC NOTE=Ref.1.
KW Direct protein sequencing.
SQ SEQUENCE 64 AA; 6990 MW; 95E063A951261830 CRC64;

Query Match 14.7%; Score 73; DB 1; Length 64;
Best Local Similarity 30.2%; Pred. No. 2.4;
Matches 19; Conservative 5; Mismatches 28; Indels 10; Gaps 3;

QY 7 CERDVQCGAGTCCALISLWRLGRLMCTPLGREGECHPGSHKVPFFRKHKHTCPLNLL 65
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
3 CGSNADCGDGCCTGGSF---NRHCQSLADGTPCQKENDYNEVKF-----GCPCKEGL 53
QY 66 LCS 68
Db :||
54 ICS 56

RESULT 4
TX16_PHONI
ID TX16_PHONI STANDARD; PRT; 68 AA.
AC P83997;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Non-toxic venom protein PRTx16C1.
OS Phoneutria nigriventer (Brazilian armed spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.
OX NCBI TaxID=6918;
RN [1]
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, MASS
RP SPECTROMETRY, AND PYRROLIDONE CARBOXYLIC ACID.
RC TISSUE=Venom;
RA Richardson M., Pimenta A.M.C., Benquerer M.P., Santoro M.M.,
RA Figueiredo S.G., Cordeiro M.N.;
RT "Non-toxic protein PRTx16C1 from venom of Brazilian armed spider
RT Phoneutria nigriventer has sequence similarities with toxins from
RT other spiders.";
RL Submitted (MAY-2004) to Swiss-Prot.
CC -!- FUNCTION: Non-toxic to mice and insects.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- MASS SPECTROMETRY: MW=7666.6; METHOD=Electrospray; RANGE=1-68;
CC NOTE=Ref.1.
KW Direct protein sequencing; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 Pyrrolidone carboxylic acid.
SQ SEQUENCE 68 AA; 7605 MW; F7DF2844EBFE5FC1 CRC64;

Query Match 14.1%; Score 70; DB 1; Length 68;
Best Local Similarity 27.5%; Pred. No. 5.3;
Matches 19; Conservative 6; Mismatches 28; Indels 16; Gaps 3;

QY 3 ITGACERDVQCGAGTCCALISLWRLGRLMCTPLGREGECHPGSHKVPFFRKHKHT- 58
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
3 IPGQSCINADCGEGCCTGGSY---NRHCQSLADGTPCQKENDYNEVKF-----GCPCKEGL 50
QY 59 CPCLPNLLC 67
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
51 CPCKEGLMC 59
```



```
RESULT 5
HEPC MORCS
ID HEPC MORCS STANDARD; PRT; 85 AA.
AC P82951
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hepcidin precursor.
OS Morone chrysops x Morone saxatilis (White bass x Striped bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Moronidae; Morone.
NCBI_TaxID=45352;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 65-85, TISSUE SPECIFICITY, ANTIBIOTIC
RP ACTIVITY, AND MASS SPECTROMETRY.
RC TISSUE=Gill, and Skin;
RX MEDLINE=21382021; PubMed=11985602;
RA Shike H., Lauch X., Westerman M.E., Ostland V.E., Carlberg J.M.,
RA Van Olst J.C., Shimizu C., Bulet P., Burns J.C.;
RT "Bass hepcidin is a novel antimicrobial peptide induced by bacterial
RT challenge.";
RL Eur. J. Biochem. 269:2232-2237(2002).
CC -!- FUNCTION: Seems to act as a signaling molecule involved in the
CC maintenance of iron homeostasis. Seems to be required in
CC conjunction with HFE to regulate both intestinal iron absorption
CC and iron storage in macrophages (By similarity).
CC -!- FUNCTION: Antimicrobial activity against Gram-negative bacteria
CC such as E.coli.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Predominantly expressed in liver.
CC -!- INDUCTION: By bacterial challenge.
CC -!- MASS SPECTROMETRY: MW=2255.97; METHOD=MALDI; RANGE=65-85;
CC NOTE=Ref.1.
CC -!- SIMILARITY: Belongs to the hepcidin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF394245; AAM28439.1; -.
CC DR EMBL; AF394246; AAM28440.1; -.
CC KW Antibiotic; Direct protein sequencing; Hormone; Signal.
CC FT SIGNAL 1 24 Potential.
CC FT PROPEP 25 64
CC FT PEPTIDE 65 85 Hepcidin.
CC FT DISULFID 66 72 Potential.
CC FT DISULFID 69 83 Potential.
CC FT DISULFID 70 82 Potential.
CC FT DISULFID 73 79 Potential.
CC SQ SEQUENCE 85 AA; 9484 MW; 0FEA55CF0A522C84 CRC64;
CC
CC Query Match 13.3%; Score 66; DB 1; Length 85;
CC Best Local Similarity 30.0%; Pred. No. 18;
CC Matches 15; Conservative 8; Mismatches 15; Indels 12; Gaps 2;
CC
CC QY 33 PLRGEGEECHPGSHKVPFFKRRKHT-----CPCLPNL-----LCSEPF 70
CC DB 36 PMSNEYQEMFVBSWKMPYNNRHRHSSPGGCRFCNCNPNMSGCGVCCRF 85
CC
CC RESULT 6
CX2X CONBE
ID CX2X CONBE STANDARD; PRT; 70 AA.
AC Q9U323;
DT 28-FEB-2003 (Rel. 41, Created)
DE Hypothetical protein YIA5A.2;
ORFNames=YIA5A.2;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Kappa-conotoxin BtX precursor.
OS Conus betulinus (Beech cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=89764;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 27-43, AND MASS SPECTROMETRY.
RC TISSUE=Venom, and Venom duct;
RX PubMed=1254781; DOI=10.1074/jbc.M210200200;
RA Fan C.-X., Chen X.-K., Zhang C., Wang L.-X., Duan K.-L., He L.-L.,
RA Cao Y., Liu S.-Y., Zhong M.-N., Ullens C., Tytgat J., Chen J.-S.,
RA Chi C.-W., Zhou Z.;
RT "A novel conotoxin from Conus betulinus, kappa-BtX, unique in cysteine
RT pattern and in function as a specific BK channel modulator.";
RL J. Biol. Chem. 278:12624-12633(2003).
CC -!- FUNCTION: Kappa-conotoxins bind and inhibit voltage-sensitive
CC potassium channels. Modulator of potassium channels, specifically
CC up-regulates the calcium and voltage-sensitive BK channels, has no
CC effect on single channel conductance, but increases the open
CC probability of BK channels.
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- PTM: Contains four disulfide bonds.
CC -!- MASS SPECTROMETRY: MW=3569; METHOD=Electrospray; RANGE=27-57;
CC NOTE=Ref.1.
CC -!- SIMILARITY: Belongs to the conotoxin O-superfamily. Kappa-type
CC family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF208661; AAF23167.1; -.
CC DR EMBL; AF208662; AAF23168.1; -.
CC KW Amidation; Cleavage on pair of basic residues;
CC Direct protein sequencing; Gamma-carboxyglutamic acid; Hydroxylation;
CC Ionic channel inhibitor; Neurotoxin; Potassium channel inhibitor;
CC Signal; Toxin; Vitamin K.
CC FT SIGNAL 1 26
CC FT CHAIN 27 57 Kappa-conotoxin BtX.
CC FT PROPEP 61 70
CC FT MOD_RES 30 30 4-carboxyglutamate.
CC FT MOD_RES 35 35 4-carboxyglutamate.
CC FT MOD_RES 44 44 4-carboxyglutamate.
CC FT MOD_RES 53 53 Hydroxyproline.
CC FT MOD_RES 57 57 Proline amide (G-58 provides amide
CC group).
CC SQ SEQUENCE 70 AA; 7900 MW; F6575A2B830AD903 CRC64;
CC
CC Query Match 12.8%; Score 63.5; DB 1; Length 70;
CC Best Local Similarity 37.3%; Pred. No. 27;
CC Matches 19; Conservative 1; Mismatches 14; Indels 17; Gaps 4;
CC
CC QY 7 CERDVQCGAGTCCATSLMLRLGRLMCTPLGREGECC-HPG--SHKVPFFPKR 54
CC DB 34 CENDSQCLNECC---W-----GGCGHPCRHPGKRLQLEFFRQR 70
CC
CC RESULT 7
Q9XXT6
ID Q9XXT6 PRELIMINARY; PRT; 83 AA.
AC Q9XXT6;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Hypothetical protein YIA5A.2;
ORFNames=YIA5A.2;
```

RESULT 9
C64AE9
ID C64AE9
PRELIMINARY;
PRT; 76 AA.


```
RC STRAIN=1;
EX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; EX2941138; CAD73029.1; -.
DR InterPro; IPR011477; DUF1584.
DR Pfam; PF07623; PEGSRP; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 76 AA; 8266 MW; B1349FB3B28D98B4 CRC64;

Query Match      11.1%; Score 55.5; DB 2; Length 76;
Best Local Similarity 33.3%; Pred. No. 2e+02;
Matches 13; Conservative 6; Mismatches 15; Indels 5; Gaps 1;

Qy 33 PLGREGECHPGS-----HKVPFFRKXKHTCTCPLNLL 66
Db 8 PPKPEPERSHPSATSLVHVHVPESKASQHRHSGFLLVNVV 46

RESULT 15
Q96S92
ID Q96S92 PRELIMINARY; PRT; 80 AA.
AC Q96S92;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li N., Zhang M., Wan T., Zhang W., Cao X.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037153; AAK67633.1; -.
KW Hypothetical protein.
SQ SEQUENCE 80 AA; 9172 MW; 4745CB6B383AB10A CRC64;

Query Match      11.1%; Score 55.5; DB 2; Length 80;
Best Local Similarity 29.4%; Pred. No. 2.1e+02;
Matches 20; Conservative 6; Mismatches 29; Indels 13; Gaps 4;

Qy 9 RDVQCGAGTCCAISLWRLRMCTPLGREGECHPGSHKVPFFRKXKHTCTCPLNLLCS 68
Db 19 QSVFCGTSTYCV-----LNTVPI--EDDHGNSNSHVKIFLPKK--LLECLPK--CS 65

Qy 69 RFPDGRYR 76
Db 66 SLPKERHR 73
```

Search completed: November 1, 2005, 15:12:19
Job time : 176 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 1, 2005, 14:52:51 ; Search time 161 Seconds
(without alignments)
206.593 Million cell updates/sec

Title: US-10-027-603-2_COPY_20_105
Perfect score: 498
Sequence: 1 AVITGACERDVCGAGTCCA.....CSRFPDGRYCRSMDLKNINF 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1117955

Minimum DB seq length: 0
Maximum DB seq length: 86

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	498	100.0	86	4 AAB70146	Aab70146 Human G p
2	498	100.0	86	5 AAB76801	Abb76801 Human ZAQ
3	498	100.0	86	5 AAB705338	Abj05338 Human ZAQ
4	498	100.0	86	5 AAO15529	Aao15529 Human phy
5	498	100.0	86	5 ABB06306	Abb06306 Human G p
6	498	100.0	86	5 AAB24383	Aae24383 Human pro
7	498	100.0	86	7 ADD69104	Add69104 Human ZAQ
8	498	100.0	86	7 ADO05360	Ado05360 Human pro
9	498	100.0	86	8 ADM43256	Adn43256 Amino aci
10	498	100.0	86	8 ADR24003	Adr24003 Human ZAQ
11	497	99.8	86	4 AAB70145	Aab70145 Human G p
12	497	99.8	86	5 AAO15528	Aao15528 Human phy
13	497	99.8	86	5 ABB06305	Abb06305 Human G p
14	497	99.8	86	7 ADD69103	Add69103 Human ZAQ
15	497	99.8	86	8 ADR24004	Adr24004 Human ZAQ
16	494	99.2	85	5 AAE24393	Aae24393 Human pro
17	478	96.0	86	5 AAE24394	Aae24394 Human pro
18	473	95.0	86	5 ABB99154	Abb99154 Rat ZAQ p
19	473	95.0	86	5 ABB06959	Abb06959 Rat G pro
20	473	95.0	86	7 ABB069160	Add69160 Rat ZAQ-r
21	473	95.0	86	8 ADM43261	Adn43261 Amino aci
22	469	94.2	86	5 ABB99156	Abb99156 Rat ZAQ p
23	469	94.2	86	5 ABB06961	Abb06961 Rat G pro
24	469	94.2	86	7 ADD69164	Add69164 Rat ZAQ-r
25	467	93.8	86	5 ABB99155	Abb99155 Rat ZAQ p

ALIGNMENTS

RESULT 1

AAB70146
ID AAB70146 standard; protein; 86 AA.
AC AAB70146;
XX
XX 29-MAY-2001 (first entry)
XX
XX Human G protein-coupled receptor protein-related sequence #2.
XX
XX Human; G protein-coupled receptor protein; nootropic; neuroprotective;
KW hypotensive; orexigenic; anti-allergic; anti-anginal; antimicrobial;
KW antibacterial; gene therapy; Alzheimer's disease; hypertension; anorexia;
KW allergy; angina pectoris; infection; MRSA;
KW multiple resistant Staphylococcus aureus.
XX Homo sapiens.
XX
XX WO200116309-A1.
XX
XX 08-MAR-2001.
XX
XX 24-AUG-2000; 2000WO-JP005685.
XX
XX 27-AUG-1999; 99JP-00241531.
XX 18-JUL-2000; 2000JP-00217474.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Watanabe T, Terao Y, Shintani Y;
PI WPI; 2001-226684/23.
XX
XX New human brain-originated guanosine triphosphate protein-coupled
PT receptor protein, its salt and encoded gene, useful in (gene) diagnosis
PT and development of preventives and remedies for Alzheimer's disease,
XX hypertension and anorexia.
XX
XX Example 4; Fig 9; 119pp; Japanese.
XX
XX The present sequence is provided in a specification relating to a protein
CC or its salt with an amino acid sequence identical or substantially
CC similar to a fully defined sequence of 393 amino acids as given in the
CC specification. The protein is useful in gene diagnosis and development of
CC preventives and remedies for diseases associated with dysfunction of the
CC protein, e.g. Alzheimer's disease, hypertension, anorexia, allergy,
CC angina pectoris and infections (e.g. multiple resistant Staphylococcus
CC aureus. The proteins and DNA encoding the proteins are also useful for

26 467 93.8 86 5 ABB06960 Rat G pro
27 467 93.8 86 7 ADD69162 Add69162 Rat ZAQ-r
28 455 91.4 86 5 ABB99149 Abb99149 Mouse ZAQ
29 455 91.4 86 7 ADD69131 Add69131 Murine ZAQ
30 455 91.4 86 7 ADO05361 Ado05361 Mouse pro
31 455 91.4 86 8 ADM43259 Adn43259 Amino aci
32 413 82.9 86 5 AAE24391 Aae24391 Human pro
33 413 82.9 86 7 ADO05372 Ado05372 PK2/PK1 c
34 413 82.9 86 8 ADM43267 Adn43267 Amino aci
35 376 75.5 81 5 AAE24390 Aae24390 Human pro
36 376 75.5 81 7 ADO05371 Ado05371 PK1/PK2 c
37 376 75.5 81 8 ADM43266 Adn43266 Amino aci
38 361 72.5 81 2 AAY11745 Aay11745 Human 5'
39 357 71.7 80 3 AAG00617 Aag00617 Human sec
40 315 63.3 80 5 ABB99160 Abb99160 PolyIepis
41 315 63.3 80 5 ABB06310 Abb06310 Dendroasp
42 315 63.3 80 7 ADD69043 Add69043 Dendroasp
43 315 63.3 80 7 ADJ71812 Adj71812 Black mam
44 315 63.3 80 7 ADO05364 Ado05364 Snake pro
45 315 63.3 80 7


```
DE Human physiologically-active ZAQ ligand-related protein 4.
XX Human; ZAQ ligand; physiologically-active ZAQ ligand; digestive disease;
KW colitis; diarrhoea.
XX Homo sapiens.
OS
PN WO200257443-A1.
XX
XX 25-JUL-2002.
XX
XX 21-JAN-2002; 2002WO-JP000378.
XX
XX 22-JAN-2001; 2001JP-00013027.
PR 17-MAY-2001; 2001JP-00147759.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Yamada T, Suenaga M, Nishimura O;
PI
XX WPI; 2002-566801/60.
XX
XX Industrial production of physiologically-active ZAQ ligand by expressing
PT in transformant prokaryote and refolding in redox buffer, for use in
PT preventing or treating digestive diseases e.g. colitis and diarrhea.
XX
XX Claim 2; Page 79; 93pp; Japanese.
XX
XX The invention comprises a method for producing an active peptide that has
CC the same activity as a ZAQ ligand isolated from eukaryotic cells. The
CC method of the invention is useful for the production of a physiologically
CC -active ZAQ ligand for use in preventing or treating digestive diseases
CC (e.g. colitis and diarrhea). The present amino acid sequence represents a
CC human physiologically active ZAQ ligand-related protein
XX
XX Sequence 86 AA;
SQ
Query Match 100.0%; Score 498; DB 5; Length 86;
Best Local Similarity 100.0%; Pred. No. 7.4e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVQCGAGTCCCAISLWLRLGLRMCTPLGREGECHPGSHKVPFFRKRKHTTCP 60
DB 1 AVITGACERDVQCGAGTCCCAISLWLRLGLRMCTPLGREGECHPGSHKVPFFRKRKHTTCP 60
QY 61 CLPNLLCSRFPPDGRYRCSMDLKNINF 86
DB 61 CLPNLLCSRFPPDGRYRCSMDLKNINF 86
RESULT 5
ID ABB06306 standard; protein; 86 AA.
XX
XX ABB06306;
AC
XX 27-MAY-2002 (first entry)
DT
XX Human G protein-coupled receptor ZAQ ligand protein SEQ ID NO:21.
DE
XX G protein-coupled receptor; ZAQ ligand; physiologically active peptide;
KW ZAQ; antidiarrheic; laxative; drug development; digestive disease;
KW colitis; diarrhoea; constipation; poor-absorption syndrome; gene therapy.
XX
XX Homo sapiens.
OS
XX WO200206483-A1.
PN
XX 24-JAN-2002.
PD
XX 17-JUL-2001; 2001WO-JP006162.
PF
XX 18-JUL-2000; 2000JP-00217442.
PR
```

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PR 02-FEB-2001; 2001JP-00026779.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Ohtaki T, Masuda Y, Takatsugu Y, Watanabe T, Terao Y, Shintani Y;
PI Hinuma S;
XX
XX WPI; 2002-188546/24.
DR N-PSDB; ABL49635.
XX
XX Physiologically-active peptides from cows milk, useful for developing
PT drugs to treat ZAQ-mediated diseases, particularly digestive diseases
PT like colitis, diarrhea, constipation and poor-absorption syndrome, by
XX gene therapy.
XX
XX Claim 1; Fig 9; 191pp; Japanese.
XX
XX The present invention describes a peptide containing an amino acid
CC sequence (I) identical to or substantially similar to that of the
CC sequences in ABB06305 or ABB06306, or its salt. (I) has antidiarrheic and
CC laxative activities. The peptides and encoding DNAs from the present
CC invention are useful for developing drugs to treat digestive diseases
CC like colitis, diarrhoea, constipation and poor-absorption syndrome,
CC including gene therapy. The physiologically-active cows milk-originated
CC peptides are applicable as a specific ligand of brain-originated orphan G
CC protein-coupled receptor protein ZAQ. ABL49615 to ABB40659 and ABB06303
CC to ABB06315 represent sequences used in the exemplification of the
CC present invention
XX
XX Sequence 86 AA;
SQ
Query Match 100.0%; Score 498; DB 5; Length 86;
Best Local Similarity 100.0%; Pred. No. 7.4e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVQCGAGTCCCAISLWLRLGLRMCTPLGREGECHPGSHKVPFFRKRKHTTCP 60
DB 1 AVITGACERDVQCGAGTCCCAISLWLRLGLRMCTPLGREGECHPGSHKVPFFRKRKHTTCP 60
QY 61 CLPNLLCSRFPPDGRYRCSMDLKNINF 86
DB 61 CLPNLLCSRFPPDGRYRCSMDLKNINF 86
RESULT 6
ID AAE24383 standard; protein; 86 AA.
XX
XX AAE24383;
AC
XX 04-OCT-2002 (first entry)
DT
XX Human prokineticin 1 mature protein.
DE
XX Human; prokineticin 1; gastrointestinal motility; intestinal cancer;
KW irritable bowel syndrome; gastrointestinal reflux disease; diarrhoea;
KW diabetic gastroparesis; chronic constipation; malabsorptive disorder;
KW inflammatory bowel disorder; analgesic; infectious disease.
XX
XX Homo sapiens.
OS
XX WO200236625-A2.
PN
XX 10-MAY-2002.
PD
XX 01-NOV-2001; 2001WO-US047969.
PF
XX 03-NOV-2000; 2000US-0245882P.
PR
XX (REGC ) UNIV CALIFORNIA.
PA
XX Zhou Q, Ehler FJ;
PI
XX
```

DR WPI; 2002-479752/51.
 DR N-PSDB; AAD39321.
 XX New isolated human prokineticin 1 and 2 polypeptides that stimulate
 PT gastrointestinal smooth muscle contraction, useful for improving impaired
 PT gastrointestinal motility in irritable bowel syndrome, chronic
 PT constipation.
 XX
 XX Claim 1; Page 79-80; 86pp; English.
 XX
 CC The invention relates to human prokineticin 1 and 2 polypeptides that
 CC stimulate gastrointestinal smooth muscle contraction and nucleic acid
 CC molecules encoding such polypeptides. Polypeptides of the invention are
 CC useful for treating disorders involving impaired gastrointestinal
 CC motility. They are useful for stimulating gastrointestinal motility in
 CC disorders such as irritable bowel syndrome, diabetic gastroparesis, post-
 CC operational ileus, chronic constipation and gastrointestinal reflux
 CC disease. The prokineticin antagonists are useful for inhibiting
 CC gastrointestinal motility in conditions of diarrhoea, malabsorptive
 CC disorders, inflammatory bowel disorders, infectious diseases and
 CC intestinal cancers. The antagonists also act as analgesics. The present
 CC sequence is human prokineticin 1 mature protein
 XX
 XX Sequence 86 AA;

Query Match 100.0%; Score 498; DB 5; Length 86;
 Best Local Similarity 100.0%; Pred. No. 7.4e-47;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AVITGACERDVQCGAGTCCATSLWLRGLRMCTPLGREGECHPGSHKVPFFFRKRKHHTCP 60
 Db 1 AVITGACERDVQCGAGTCCATSLWLRGLRMCTPLGREGECHPGSHKVPFFFRKRKHHTCP 60

QY 61 CLPNLLCSRFDPGRYRCSDMLKNINF 86
 Db 61 CLPNLLCSRFDPGRYRCSDMLKNINF 86

RESULT 7
 ADD69104
 ID ADD69104 standard; protein; 86 AA.

AC ADD69104;
 XX
 XX 15-JAN-2004 (first entry)
 DT
 XX Human ZAQ-related protein - SEQ ID 82.
 DE
 XX angiogenesis inhibitor; cytostatic; antiinflammatory; cancer;
 KW ovarian disease; diabetic retinopathy; inflammatory; ZAQ; Bv8; I5E;
 KW human.
 XX

OS Homo sapiens.

XX WO2003066860-A1.

XX 14-AUG-2003.

XX 03-FEB-2003; 2003WO-JP001057.

XX 04-FEB-2002; 2002JP-00027299.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Ohtaki T, Masuda Y, Takatsu Y;

DR WPI; 2003-646310/61.

DR N-PSDB; ADD69110.

XX Angiogenesis inhibitors for treatment and prevention of cancer, ovarian

PT diseases and inflammatory disease.

XX Claim 1; SEQ ID NO 82; 308pp; Japanese.

PS

XX The invention relates to a novel angiogenesis inhibitor comprising a
 CC compound that inhibits the activity of an amino acid sequence given in
 CC the specification. Angiogenesis-related proteins Bv8, ZAQ and I5E were
 CC utilised within the method of the invention. The molecules of the
 CC invention demonstrate cytostatic and antiinflammatory activities whilst
 CC the method may be useful for treatment and prevention of cancer, ovarian
 CC diseases, diabetic retinopathy and inflammatory disease. The current
 CC sequence is that of the human ZAQ-related protein of the invention.
 XX
 XX Sequence 86 AA;

Query Match 100.0%; Score 498; DB 7; Length 86;
 Best Local Similarity 100.0%; Pred. No. 7.4e-47;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCATSLWLRGLRMCTPLGREGECHPGSHKVPFFFRKRKHHTCP 60
 Db 1 AVITGACERDVQCGAGTCCATSLWLRGLRMCTPLGREGECHPGSHKVPFFFRKRKHHTCP 60

QY 61 CLPNLLCSRFDPGRYRCSDMLKNINF 86

Db 61 CLPNLLCSRFDPGRYRCSDMLKNINF 86

RESULT 8
 ADO05360
 ID ADO05360 standard; protein; 86 AA.

XX ADO05360;

XX 01-JUL-2004 (first entry)

XX Human prokineticin 1 (PK1), SEQ ID NO:9.

DE Human prokineticin 1; PK1; circadian rhythm; modulation; drug screening;
 XX circadian rhythm disorder; non-24-hour sleep-wake syndrome;
 KW rapid time-zone change syndrome; jetlag; work-shift syndrome;
 KW delayed phase sleep syndrome; advanced sleep phase syndrome;
 KW irregular sleep-wake pattern syndrome; decreased amplitude syndrome;
 KW seasonal affective disorder; ultradian rhythm; daydreaming; urination;
 KW hunger; infaridian rhythm; female sexual receptivity; CNS;
 KW central nervous syndrome; PK2 receptor antagonist; PK2 receptor agonist.
 XX

OS Homo sapiens.

XX WO2003088904-A2.

XX 30-OCT-2003.

XX 15-APR-2003; 2003WO-US011538.

XX 15-APR-2002; 2002US-0372836P.

XX (REGC) UNIV CALIFORNIA.

XX Zhou Q, Bullock CM;

XX WPI; 2003-854028/79.

XX Screening for compounds for modulating circadian rhythm, for treating
 PT seasonal disorders, comprises determining ability of prokineticin-2
 PT receptor antagonist or agonist to modulate one or more circadian rhythm
 PT function indicia.

XX Disclosure; SEQ ID NO 9; 164pp; English.

XX The invention relates to a method of screening for a compound for its
 CC ability to modulate circadian rhythm. The method involved determining the
 CC ability of a prokineticin 2 (PK2) receptor agonist or antagonist to
 CC modulate one or more indicia or circadian rhythm function. The compound
 CC is identified as being a PK2 receptor agonist or antagonist by
 CC determining its effect on a predetermined signal such as calcium


```
XX WPI; 2004-593431/57.
XX
XX New monoclonal antibody having high avidity to human ZAQ1-1 polypeptide,
XX useful for preventing, treating or diagnosing diseases such as
XX endometrial cancer, ovulation disorders, Alzheimer's disease, AIDS,
XX Parkinson's disease and diabetes.
XX
XX Claim 1; SEQ ID NO 1; 64pp; Japanese.
XX
XX The invention relates to a monoclonal antibody (I) having high avidity to
XX human ZAQ1-1 ligand polypeptides, comprising either of two fully defined
XX sequences of 86 amino acids (S1). (I) is ZLI-107a or ZLI-234a produced
XX from hybridoma cells ZLI-107 FERM BP-8256 or ZLI-234 FERM BP-8257. (I) is
XX useful for carrying out assay of the polypeptide containing (S1) which
XX involves reacting (I) with the test-liquid containing the polypeptide or
XX its salt, and measuring the ratio of the polypeptide bound to (I). (I) is
XX useful as a diagnostic or therapeutic agent for diagnosis and/or
XX treatment of diseases such as endometrial cancer, endometriosis or
XX ovulation disorders, digestive diseases, diseases associated with
XX angiogenesis, diseases relating to pregnancy, eating disorder, sleeping
XX disorder, seasonal depression, reproductive dysfunction, endocrine
XX diseases, senile dementia, Alzheimer's disease, various disorders caused
XX by aging, cerebral circulatory disorder, head trauma, spinal injury,
XX epilepsy, anxiety, depression, manic depression, schizophrenia,
XX alcoholism, Parkinson's disease, hypertension, arteriosclerosis,
XX arrhythmia, premenstrual disorder syndrome, glaucoma, AIDS, diabetes,
XX etc. This sequence corresponds to a ZAQ-1 ligand used in the invention.
XX
XX Sequence 86 AA;
SQ
Query Match 100.0%; Score 498; DB 8; Length 86;
Best Local Similarity 100.0%; Pred. No. 7.4e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVQCGAGTCCATSLWLRLGRLMCTPLGREGECHPGSHKVPFFFRKHKHTCP 60
DB 1 AVITGACERDVQCGAGTCCATSLWLRLGRLMCTPLGREGECHPGSHKVPFFFRKHKHTCP 60
QY 61 CLPNLLCSRFDPGRYRCSDMLKNINF 86
DB 61 CLPNLLCSRFDPGRYRCSDMLKNINF 86
RESULT 11
ID AAB70145
AC AAB70145
XX
XX 29-MAY-2001 (first entry)
XX
XX Human G protein-coupled receptor protein-related sequence #1.
XX
XX Human; G protein-coupled receptor protein; nootropic; neuroprotective;
XX hypertensive; orexigenic; antiallergic; antianginal; antimicrobial;
XX antibacterial; gene therapy; Alzheimer's disease; hypertension; anorexia;
XX allergy; angina pectoris; infection; MRSA;
XX multiple resistant Staphylococcus aureus.
XX
XX Homo sapiens.
XX
XX WO200116309-A1.
XX
XX 08-MAR-2001.
XX
XX 24-AUG-2000; 2000WO-JP005685.
XX
XX 27-AUG-1999; 99JP-00241531.
XX
XX 18-JUL-2000; 2000JP-00217474.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX PA
XX
XX The invention comprises a method for producing an active peptide that has
```

```
PI Watanabe T, Terao Y, Shintani Y;
XX
XX WPI; 2001-226684/23.
XX
XX New human brain-originated guanosine triphosphate protein-coupled
XX receptor protein, its salt and encoded gene, useful in (gene) diagnosis
XX and development of preventives and remedies for Alzheimer's disease,
XX hypertension and anorexia.
XX
XX Example 4; Fig 9; 119pp; Japanese.
XX
XX The present sequence is provided in a specification relating to a protein
XX or its salt with an amino acid sequence identical or substantially
XX similar to a fully defined sequence of 393 amino acids as given in the
XX specification. The protein is useful in gene diagnosis and development of
XX preventives and remedies for diseases associated with dysfunction of the
XX protein, e.g. Alzheimer's disease, hypertension, anorexia, allergy,
XX angina pectoris and infections (e.g. multiple resistant Staphylococcus
XX aureus). The proteins and DNA encoding the proteins are also useful for
XX the treatment of these diseases by gene therapy
XX
XX Sequence 86 AA;
SQ
Query Match 99.8%; Score 497; DB 4; Length 86;
Best Local Similarity 98.8%; Pred. No. 9.5e-47;
Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVQCGAGTCCATSLWLRLGRLMCTPLGREGECHPGSHKVPFFFRKHKHTCP 60
DB 1 AVITGACERDVQCGAGTCCATSLWLRLGRLMCTPLGREGECHPGSHKVPFFFRKHKHTCP 60
QY 61 CLPNLLCSRFDPGRYRCSDMLKNINF 86
DB 61 CLPNLLCSRFDPGRYRCSDMLKNINF 86
RESULT 12
ID AAO15528
XX
XX AAO15528 standard; protein; 86 AA.
XX
XX AAO15528;
XX
XX 24-OCT-2002 (first entry)
XX
XX Human physiologically-active ZAQ ligand-related protein 3.
XX
XX Human; ZAQ ligand; physiologically-active ZAQ ligand; digestive disease;
XX colitis; diarrhoea.
XX
XX Homo sapiens.
XX
XX WO200257443-A1.
XX
XX 25-JUL-2002.
XX
XX 21-JAN-2002; 2002WO-JP000378.
XX
XX 22-JAN-2001; 2001JP-00013027.
XX
XX 17-MAY-2001; 2001JP-00147759.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Yamada T, Suenaga M, Nishimura O;
XX
XX WPI; 2002-566801/60.
XX
XX Industrial production of physiologically-active ZAQ ligand by expressing
XX in transformant prokaryote and refolding in redox buffer, for use in
XX preventing or treating digestive diseases e.g. colitis and diarrhea.
XX
XX Claim 4; Page 78; 93pp; Japanese.
XX
XX The invention comprises a method for producing an active peptide that has
```

CC the same activity as a ZAQ ligand isolated from eukaryotic cells. The
CC method of the invention is useful for the production of a physiologically
CC -active ZAQ ligand for use in preventing or treating digestive diseases
CC (e.g. colitis and diarrhea). The present amino acid sequence represents a
CC human physiologically active ZAQ ligand-related protein
XX

SQ Sequence 86 AA;

Query Match 99.8%; Score 497; DB 5; Length 86;
Best Local Similarity 98.8%; Pred. No. 9.5e-47;
Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGECHPGSHKVPFRRKRKHTCP 60
DB 1 AVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGECHPGSHKVPFRRKRKHTCP 60

QY 61 CLPNLCSRFPPDGRYRCSMDLNINF 86
DB 61 CLPNLCSRFPPDGRYRCSMDLNINF 86

RESULT 13

ABB06305
ID ABB06305 standard; protein; 86 AA.

XX
AC ABB06305;

XX 27-MAY-2002 (first entry)

XX Human G protein-coupled receptor ZAQ ligand protein SEQ ID NO:20.

XX G protein-coupled receptor; ZAQ ligand; physiologically active peptide;
KW ZAQ; antidiarrheic; laxative; drug development; digestive disease;
KW colitis; diarrhoea; constipation; poor-absorption syndrome; gene therapy.

XX Homo sapiens.

XX WO200206483-A1.

XX 24-JAN-2002.

XX 17-JUL-2001; 2001WO-JP006162.

XX 18-JUL-2000; 2000JP-00217442.

XX 02-FEB-2001; 2001JP-00026779.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Ohtaki T, Masuda Y, Takatsu Y, Watanabe T, Teraso Y, Shintani Y,
PI Hinuma S;

XX WPI; 2002-188546/24.

XX N-PSDB; ABL49634.

XX Physiologically-active peptides from cows milk, useful for developing
PT drugs to treat ZAQ-mediated diseases, particularly digestive diseases
PT like colitis, diarrhea, constipation and poor-absorption syndrome, by
PT gene therapy.

XX Claim 1; Fig 9; 191pp; Japanese.

XX The present invention describes a peptide containing an amino acid
CC sequence (I) identical to or substantially similar to that of the
CC sequences in ABB06305 or ABB06306, or its salt. (I) has antidiarrheic and
CC laxative activities. The peptides and encoding DNAs from the present
CC invention are useful for developing drugs to treat digestive diseases
CC like colitis, diarrhoea, constipation and poor-absorption syndrome,
CC including gene therapy. The physiologically-active cows milk-originated
CC peptides are applicable as a specific ligand of brain-originated orphan G
CC protein-coupled receptor protein ZAQ. ABL49615 to ABB40659 and ABB06303
CC to ABB06315 represent sequences used in the exemplification of the
CC present invention

SQ Sequence 86 AA;

Query Match 99.8%; Score 497; DB 5; Length 86;
Best Local Similarity 98.8%; Pred. No. 9.5e-47;
Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGECHPGSHKVPFRRKRKHTCP 60
DB 1 AVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGECHPGSHKVPFRRKRKHTCP 60

QY 61 CLPNLCSRFPPDGRYRCSMDLNINF 86
DB 61 CLPNLCSRFPPDGRYRCSMDLNINF 86

RESULT 14

ADD69103
ID ADD69103 standard; protein; 86 AA.

XX
AC ADD69103;

XX 15-JAN-2004 (first entry)

XX Human ZAQ-related protein - SEQ ID 81.

XX angiogenesis inhibitor; cytostatic; antiinflammatory; cancer;
KW ovarian disease; diabetic retinopathy; inflammatory; ZAQ; Bv8; 15E;
KW human.

XX Homo sapiens.

XX WO2003066860-A1.

XX 14-AUG-2003.

XX 03-FEB-2003; 2003WO-JP001057.

XX 04-FEB-2002; 2002JP-00027299.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Ohtaki T, Masuda Y, Takatsu Y;

XX WPI; 2003-646310/61.

XX N-PSDB; ADD69109.

XX Angiogenesis inhibitors for treatment and prevention of cancer, ovarian
PT diseases and inflammatory disease.

XX Claim 1; SEQ ID NO 81; 308pp; Japanese.

XX The invention relates to a novel angiogenesis inhibitor comprising a
CC compound that inhibits the activity of an amino acid sequence given in
CC the specification. Angiogenesis-related proteins Bv8, ZAQ and 15E were
CC utilised within the method of the invention. The molecules of the
CC invention demonstrate cytostatic and antiinflammatory activities whilst
CC the method may be useful for treatment and prevention of cancer, ovarian
CC diseases, diabetic retinopathy and inflammatory disease. The current
CC sequence is that of the human ZAQ-related protein of the invention.

XX Sequence 86 AA;

Query Match 99.8%; Score 497; DB 7; Length 86;
Best Local Similarity 98.8%; Pred. No. 9.5e-47;
Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGECHPGSHKVPFRRKRKHTCP 60
DB 1 AVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGECHPGSHKVPFRRKRKHTCP 60

QY 61 CLPNLCSRFPPDGRYRCSMDLNINF 86
DB 61 CLPNLCSRFPPDGRYRCSMDLNINF 86

RESULT 15
ADR24004
ID ADR24004 standard; protein; 86 AA.
XX
AC ADR24004;
XX
DT 21-OCT-2004 (first entry)
XX
DE Human ZAQ-1 ligand protein #2.
XX
KW antiangiogenic; antialcoholic; antiarrhythmic; antiarteriosclerotic;
KW anticonvulsant; antidepressant; antidiabetic; anti-HIV; antimanic;
KW antiparkinsonian; cerebroprotective; cyostatic; eating disorders;
KW endocrine; gastrointestinal; gynecological; hypnotic; hypotensive;
KW neuroleptic; neuroprotective; nootropic; ophthalmological; tranquilizer;
KW vasotropic; vulnary; monoclonal antibody; human; ZAQ-1; ligand;
KW hybridoma cell; assay; diagnosis; endometrial cancer; endometriosis;
KW ovulation disorder; digestive disease; angiogenesis; pregnancy;
KW eating disorder; sleeping disorder; seasonal depression;
KW reproductive dysfunction; endocrine disease; senile dementia;
KW Alzheimer's disease; aging; cerebral circulatory disorder; head trauma;
KW spinal injury; epilepsy; anxiety; depression; schizophrenia; alcoholism;
KW Parkinson's disease; hypertension; arteriosclerosis; arrhythmia;
KW premenstrual disorder syndrome; glaucoma; AIDS; diabetes.
XX
OS Homo sapiens.
XX
PN WO2004065419-A1.
XX
PD 05-AUG-2004.
XX
PF 21-JAN-2004; 2004WO-JP000498.
XX
PR 22-JAN-2003; 2003JP-00014055.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Matsumoto H, Horikoshi Y, Masuda Y, Ohtaki T;
XX
DR WPI; 2004-593431/57.
XX
PT New monoclonal antibody having high avidity to human ZAQ-1 polypeptide,
PT useful for preventing, treating or diagnosing diseases such as
PT endometrial cancer, ovulation disorders, Alzheimer's disease, AIDS,
PT Parkinson's disease and diabetes.
XX
PS Claim 1; SEQ ID NO 2; 64pp; Japanese.
XX
CC The invention relates to a monoclonal antibody (I) having high avidity to
CC human ZAQ-1 ligand polypeptides, comprising either of two fully defined
CC sequences of 86 amino acids (S1). (I) is ZLI-107a or ZLI-234a produced
CC from hybridoma cells ZLI-107 FERM BP-8256 or ZLI-234 FERM BP-8257. (I) is
CC useful for carrying out assay of the polypeptide containing (S1) which
CC involves reacting (I) with the test-liquid containing the polypeptide or
CC its salt, and measuring the ratio of the polypeptide bound to (I). (I) is
CC useful as a diagnostic or therapeutic agent for diagnosis and/or
CC treatment of diseases such as endometrial cancer, endometriosis or
CC ovulation disorders, digestive diseases, diseases associated with
CC angiogenesis, diseases relating to pregnancy, eating disorder, sleeping
CC disorder, seasonal depression, reproductive dysfunction, endocrine
CC diseases, senile dementia, Alzheimer's disease, various disorders caused
CC by aging, cerebral circulatory disorder, head trauma, spinal injury,
CC epilepsy, anxiety, depression, manic depression, schizophrenia,
CC alcoholism, Parkinson's disease, hypertension, arteriosclerosis,
CC arrhythmia, premenstrual disorder syndrome, glaucoma, AIDS, diabetes,
CC etc. This sequence corresponds to a ZAQ-1 ligand used in the invention.
XX
SQ Sequence 86 AA;

Query Match 99.8%; Score 497; DB 8; Length 86;
Best Local Similarity 98.8%; Pred. No. 9.5e-47;

Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLRGEGECHPGSHKVPFFRKRKHTCP 60
Db 1 AVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLRGEGECHPGSHKVPFFRKRKHTCP 60
Qy 61 CLPNLLCSRFPDGRYRCMDLKNINF 86
Db 61 CLPNLLCSRFPDGRYRCMDLKNINF 86

Search completed: November 1, 2005, 15:09:17
Job time : 163 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 1, 2005, 15:03:42 ; Search time 42 Seconds
(without alignments)
152.853 Million cell updates/sec

Title: US-10-027-603-2_COPY_20_105
Perfect score: 498
Sequence: 1 AVITGACERDVQCGAGTCA.....CSRFPDGRYCRSMDLKNINF 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 312316

Minimum DB seq length: 0
Maximum DB seq length: 86

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCITUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	357	71.7	80	US-09-513-999C-4698	Sequence 4698, Ap
2	64.5	13.0	77	US-08-866-545-2	Sequence 2, Appli
3	64.5	13.0	77	US-09-627-775-2	Sequence 2, Appli
4	56.5	11.3	79	US-10-006-011A-7	Sequence 7, Appli
5	55.5	11.1	44	US-08-050-319B-37	Sequence 37, Appl
6	55.5	11.1	44	US-08-465-982-37	Sequence 37, Appl
7	55.5	11.1	80	US-09-621-976-7198	Sequence 6198, Ap
8	52.5	10.5	69	US-09-480-251-6	Sequence 6, Appli
9	52.5	10.5	70	US-09-480-251-6	Sequence 2, Appli
10	52	10.4	36	PCR-US96-01720-2	Sequence 2, Appli
11	52	10.4	43	US-09-894-882-233	Sequence 233, App
12	52	10.4	43	US-09-894-882-260	Sequence 260, App
13	52	10.4	43	US-09-894-882-266	Sequence 266, App
14	52	10.4	43	US-09-894-882-272	Sequence 272, App
15	52	10.4	63	US-09-894-882-347	Sequence 347, App
16	51.5	10.3	74	US-09-270-767-34440	Sequence 34440, A
17	51.5	10.3	74	US-09-270-767-49657	Sequence 49657, A
18	51	10.2	43	US-09-894-882-483	Sequence 483, App
19	51	10.2	43	US-09-894-882-484	Sequence 484, App
20	51	10.2	43	US-09-894-882-487	Sequence 487, App
21	51	10.2	69	US-09-894-882-232	Sequence 232, App
22	51	10.2	69	US-09-894-882-259	Sequence 259, App
23	51	10.2	69	US-09-894-882-271	Sequence 271, App
24	50.5	10.1	72	US-09-270-767-41152	Sequence 41152, A
25	50.5	10.1	72	US-09-270-767-56368	Sequence 56368, A
26	50.5	10.1	77	US-08-264-534-1	Sequence 1, Appli
27	50.5	10.1	77	US-08-083-590A-14	Sequence 14, Appli

28	50.5	10.1	77	1	US-08-465-500-1	Sequence 1, Appli
29	50.5	10.1	77	2	US-08-346-126-1	Sequence 1, Appli
30	50.5	10.1	77	2	US-08-346-128-1	Sequence 1, Appli
31	50.5	10.1	77	3	US-08-532-384-14	Sequence 14, Appli
32	50.5	10.1	77	3	US-08-893-828-1	Sequence 1, Appli
33	50	10.0	43	4	US-09-894-882-269	Sequence 269, App
34	50	10.0	43	4	US-09-894-882-485	Sequence 485, App
35	50	10.0	48	3	US-08-665-259-6	Sequence 6, Appli
36	50	10.0	48	3	US-08-762-500-6	Sequence 6, Appli
37	50	10.0	49	3	US-08-665-259-5	Sequence 5, Appli
38	50	10.0	49	3	US-08-762-500-5	Sequence 5, Appli
39	50	10.0	69	4	US-09-894-882-265	Sequence 265, App
40	50	10.0	70	4	US-09-894-882-353	Sequence 353, App
41	49.5	9.9	47	1	US-08-377-687-28	Sequence 28, Appl
42	49.5	9.9	47	1	US-08-656-318A-13	Sequence 13, Appl
43	49.5	9.9	47	2	US-08-777-192-28	Sequence 28, Appl
44	49.5	9.9	47	2	US-08-956-459-13	Sequence 13, Appl
45	49.5	9.9	47	3	US-08-971-982-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1

US-09-513-999C-4698
; Sequence 4698, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4698
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SIGNAL
; LOCATION: -19 -1
; OTHER INFORMATION: score 7.2
; OTHER INFORMATION: seq VSIMLLLVTVSDC/AV
US-09-513-999C-4698

Query Match 71.7%; Score 357; DB 4; Length 80;
Best Local Similarity 98.4%; Pred. No. 1e-34; 0; Indels 0; Gaps 0;
Matches 60; Conservative 1; Mismatches 0

Qy	1	AVITGACERDVQCGAGTCAISLWLRGRLMCTPLGRGEGCHPGSHKVPFFRKRKHTCP	60
Db	20	AVITGACERDVQCGAGTCAISLWLRGRLMCTPLGRGEGCHPGSHKIPFFRKRKHTCP	79
Qy	61	C 61	
Db	80	C 80	

RESULT 2

US-08-866-545-2
; Sequence 2, Application US/08866545
; Patent No. 6265535
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; APPLICANT: Murali, Ramachandran
; APPLICANT: Takasaki, Wataru
; TITLE OF INVENTION: PEPTIDES AND PEPTIDE

;; TITLE OF INVENTION: ANALOGUES DESIGNED FROM BINDING SITES OF TUMOR
;; TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR SUPERFAMILY AND THEIR
;; TITLE OF INVENTION: US95
;; NUMBER OF SEQUENCES: 27
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds LLP
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: NY
;; COUNTRY: USA
;; ZIP: 10036-2811
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: Fast-SEQ Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/866,545
;; FILING DATE: 30-MAY-1997
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Coruzzi, Laura A
;; REGISTRATION NUMBER: 30,742
;; REFERENCE/DOCKET NUMBER: 009113-0004-999
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-493-4935
;; TELEFAX: 650-493-5556
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 77 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: No. 6265535e
US-08-866-545-2

Query Match 13.0%; Score 64.5; DB 3; Length 77;
Best Local Similarity 38.3%; Pred. No. 2.5;
Matches 18; Conservative 4; Mismatches 16; Indels 9; Gaps 3;

QY 2 VITGACERD----VQCGAGTCCALSILWLRLMCTPLRGEGEECHPG 44
DB 32 VETQACTREQNRICTCRPGWYCALSK-QEGCRLCAPL-----RKCRPG 73

RESULT 3

;; Sequence 2, Application US/09627775
;; Patent No. 6682739
;; GENERAL INFORMATION:
;; APPLICANT: Greene, Mark
;; APPLICANT: Murali, Ramachandran
;; APPLICANT: Aoki, Kazuhiro
;; APPLICANT: Baron, Roland
;; TITLE OF INVENTION: Methods of Inhibiting Osteoclastogenesis
;; FILE REFERENCE: UPN3832
;; CURRENT APPLICATION NUMBER: US/09/627,775
;; CURRENT FILING DATE: 2000-07-28
;; PRIOR APPLICATION NUMBER: 60/146,090
;; PRIOR FILING DATE: 1999-07-28
;; NUMBER OF SEQ ID NOS: 29
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 2
;; LENGTH: 77
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-627-775-2

Query Match 13.0%; Score 64.5; DB 4; Length 77;

Best Local Similarity 38.3%; Pred. No. 2.5;
Matches 18; Conservative 4; Mismatches 16; Indels 9; Gaps 3;
QY 2 VITGACERD----VQCGAGTCCALSILWLRLMCTPLRGEGEECHPG 44
DB 32 VETQACTREQNRICTCRPGWYCALSK-QEGCRLCAPL-----RKCRPG 73

RESULT 4

US-10-006-011A-7
;; Sequence 7, Application US/10006011A
;; Patent No. 6821947
;; GENERAL INFORMATION:
;; APPLICANT: Iozzo, Renato V.
;; TITLE OF INVENTION: Endorepellin: methods and compositions
;; TITLE OF INVENTION: for inhibiting angiogenesis
;; FILE REFERENCE: 8321-95
;; CURRENT APPLICATION NUMBER: US/10/006,011A
;; CURRENT FILING DATE: 2001-12-04
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: FastSEQ for Windows Version 4.0
;; SEQ ID NO 7
;; LENGTH: 79
;; TYPE: PRT
;; ORGANISM: human
US-10-006-011A-7

Query Match 11.3%; Score 56.5; DB 4; Length 79;
Best Local Similarity 30.3%; Pred. No. 22;
Matches 23; Conservative 4; Mismatches 36; Indels 13; Gaps 4;

QY 9 RDVCGAGTCCALSILWLRLMCTPLRGEGEECHPGSHKVPFFRKRKHTCP--CLPNLL 66
DB 2 RDRPCQGGQCHDSSESYVCVC-PAGFTGSRCE-----HSQALHCHPEACGPDAT 51

QY 67 CSRFPDGR-YRCSMDL 81

DB 52 CVNRPDGRGYTCRCHL 67

RESULT 5

US-08-050-319B-37
;; Sequence 37, Application US/08050319B
;; Patent No. 5633145
;; GENERAL INFORMATION:
;; APPLICANT: M.Feldmann, P.W. Gray,
;; APPLICANT: M.J.C. Turner, F.M.Brennan
;; TITLE OF INVENTION: Modified human TNFalpha (Tumor
;; TITLE OF INVENTION: Necrosis Factor alpha) Receptor
;; NUMBER OF SEQUENCES: 57
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Reed & Robbins
;; STREET: 635 Bryant Street
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94301
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/050,319B
;; FILING DATE: 10-May-1993
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Robbins, Roberta L.
;; REGISTRATION NUMBER: 33,208
;; REFERENCE/DOCKET NUMBER: 5150-0030
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 617-8999
;; TELEFAX: (415) 327-3231

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 44 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-050-3198-37

Query Match 11.1%; Score 55.5; DB 1; Length 44;

Best Local Similarity 40.6%; Pred. No. 15;

Matches 13; Conservative 3; Mismatches 11; Indels 5; Gaps 2;

QY 13 CGAGTCCCAISLWRLGRLMCTPLGREGECHPG 44

DB 2 CRPGWCALSK-QEGCRLCAPL----RKCRPG 28

RESULT 6

US-08-465-982-37

Sequence 37, Application US/08465982

Patent No. 5863786

GENERAL INFORMATION:

APPLICANT: M. Feldmann, P. W. Gray,

APPLICANT: M.J.C. Turner, F.M. Brennan

TITLE OF INVENTION: Modified human TNFalpha (Tumor

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Reed & Robbins

STREET: 635 Bryant Street

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/465,982

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/050,319

FILING DATE: 10-May-1993

ATTORNEY/AGENT INFORMATION:

NAME: Robbins, Roberta L.

REGISTRATION NUMBER: 33,208

REFERENCE/DOCKET NUMBER: 5150-0030

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 617-8999

TELEFAX: (415) 327-3231

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 44 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-465-982-37

Query Match 11.1%; Score 55.5; DB 2; Length 44;

Best Local Similarity 40.6%; Pred. No. 15;

Matches 13; Conservative 3; Mismatches 11; Indels 5; Gaps 2;

QY 13 CGAGTCCCAISLWRLGRLMCTPLGREGECHPG 44

DB 2 CRPGWCALSK-QEGCRLCAPL----RKCRPG 28

RESULT 7

US-09-621-976-7198

Sequence 7198, Application US/09621976

Patent No. 6639063

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Jobert, S.Y.

TITLE OF INVENTION: ESTs and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 7198

LENGTH: 80

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: UNSURE

LOCATION: 74

OTHER INFORMATION: Xaa = *, Trp

US-09-621-976-7198

Query Match 11.1%; Score 55.5; DB 4; Length 80;

Best Local Similarity 29.4%; Pred. No. 30;

Matches 20; Conservative 6; Mismatches 29; Indels 13; Gaps 4;

QY 9 RDVQCGAGTCCCAISLWRLGRLMCTPLGREGECHPGSKVFFRKRRKHTCPCLPNLLCS 68

DB 19 QSVFCGTSTYCV-----LNTVPPI--EDDHGNSNSHVKIFLPKK--LLECLPK--CS 65

QY 69 RFPDGRYR 76

DB 66 SLPKERHR 73

RESULT 8

US-09-480-251-6

Sequence 6, Application US/09480251

Patent No. 6465719

GENERAL INFORMATION:

APPLICANT: DeRose, Richard

APPLICANT: Freysinet, Georges

TITLE OF INVENTION: Chimeric Gene Encoding Drosomycin,

TITLE OF INVENTION: Vector Containing It And Production Of Disease-Resistant

TITLE OF INVENTION: Transgenic Plants

FILE REFERENCE: A32889-PCT-USA-A

CURRENT APPLICATION NUMBER: US/09/480,251

CURRENT FILING DATE: 2000-01-11

PRIOR APPLICATION NUMBER: PCT/FR98/01462

PRIOR FILING DATE: 1998-07-08

PRIOR APPLICATION NUMBER: FRANCE 97/09,115

PRIOR FILING DATE: 1997-07-11

PRIOR APPLICATION NUMBER: FRANCE 9709,663

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 6

LENGTH: 69

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: The ubiquitin - drosomycin fusion peptide

Query Match 10.5%; Score 52.5; DB 4; Length 69;

Best Local Similarity 34.0%; Pred. No. 57;

Matches 16; Conservative 4; Mismatches 20; Indels 7; Gaps 3;

QY 2 VITGACERDVQCGAGTC---CAISLWRLGL--RMCTPLGREGECHP 43

DB 16 VILGANEADADCLSGRYKGCFAV--WDNETCRVCKEGRSSGHCSP 60

Query Match 10.4%; Score 52; DB 5; Length 36;
Best Local Similarity 35.7%; Pred. No. 32;

; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma C.
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 347
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Conus striolatus
US-09-894-882-347

Query Match 10.4%; Score 52; DB 4; Length 63;
Best Local Similarity 31.9%; Pred.No. 59;
Matches 15; Conservative 5; Mismatches 13; Indels 14; Gaps 3;

QY 2 VITGACERDVQCGAGTCCA-ISLWLRGLRMCTPLGREGECHPGSHK 47
Db 19 VLTNACHMD--CSKWTCCSGICCFYCGRPMC-----PGTRR 52

Search completed: November 1, 2005, 15:14:00
Job time : 51 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 1, 2005, 15:12:34 ; Search time 164 Seconds
(without alignments)
219.218 Million cell updates/sec

Title: US-10-027-603-2_COPY_20_105
Perfect score: 498
Sequence: 1 AVITGACRDRVCGAGTCCA.....CSRFPDGRYRCMDLKNINF 86

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1865214 seqs, 418043040 residues

Total number of hits satisfying chosen parameters: 770794

Minimum DB seq length: 0
Maximum DB seq length: 86

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
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2	498	100.0	86 14 US-10-323-157-3	Sequence 3, Appli
3	498	100.0	86 15 US-10-417-426-9	Sequence 9, Appli
4	498	100.0	86 15 US-10-333-192-21	Sequence 21, Appli
5	498	100.0	86 16 US-10-680-554-5	Sequence 5, Appli
6	498	100.0	86 16 US-10-713-567-3	Sequence 3, Appli
7	498	100.0	86 17 US-10-811-328-3	Sequence 3, Appli
8	498	100.0	86 17 US-10-912-907-3	Sequence 3, Appli
9	498	100.0	86 17 US-10-415-724-3	Sequence 3, Appli
10	498	100.0	86 18 US-10-871-152-22	Sequence 22, Appli
11	498	100.0	86 18 US-10-503-554A-82	Sequence 82, Appli

12	498	100.0	86 18 US-10-343-095A-117	Sequence 117, Appl
13	497	99.8	86 15 US-10-333-192-20	Sequence 20, Appl
14	497	99.8	86 18 US-10-503-554A-81	Sequence 81, Appl
15	494	99.2	85 13 US-10-016-481-16	Sequence 16, Appl
16	494	99.2	85 14 US-10-323-157-16	Sequence 16, Appl
17	494	99.2	85 16 US-10-713-567-16	Sequence 16, Appl
18	494	99.2	85 17 US-10-811-328-16	Sequence 16, Appl
19	494	99.2	85 17 US-10-912-907-16	Sequence 16, Appl
20	494	99.2	85 17 US-10-415-724-16	Sequence 16, Appl
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26	478	96.0	86 17 US-10-811-328-17	Sequence 17, Appl
27	478	96.0	86 17 US-10-912-907-17	Sequence 17, Appl
28	478	96.0	86 17 US-10-415-724-17	Sequence 17, Appl
29	476	95.6	82 18 US-10-977-113-11	Sequence 11, Appl
30	473	95.0	86 15 US-10-470-951-37	Sequence 37, Appl
31	473	95.0	86 16 US-10-362-504-49	Sequence 49, Appl
32	473	95.0	86 16 US-10-680-554-10	Sequence 10, Appl
33	473	95.0	86 16 US-10-713-567-30	Sequence 30, Appl
34	473	95.0	86 17 US-10-811-328-30	Sequence 30, Appl
35	473	95.0	86 18 US-10-503-554A-138	Sequence 138, Appl
36	469	94.2	86 15 US-10-470-951-41	Sequence 41, Appl
37	469	94.2	86 16 US-10-362-504-53	Sequence 53, Appl
38	469	94.2	86 18 US-10-503-554A-142	Sequence 142, Appl
39	467	93.8	86 15 US-10-470-951-39	Sequence 39, Appl
40	467	93.8	86 16 US-10-362-504-51	Sequence 51, Appl
41	467	93.8	86 18 US-10-503-554A-140	Sequence 140, Appl
42	455	91.4	86 15 US-10-417-426-10	Sequence 10, Appl
43	455	91.4	86 15 US-10-470-951-8	Sequence 8, Appli
44	455	91.4	86 16 US-10-680-554-8	Sequence 8, Appli
45	455	91.4	86 16 US-10-713-567-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-10-016-481-3
; Sequence 3, Application US/10016481
; Publication No. US20020115610A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Ehler, Frederick
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; TITLE OF INVENTION: Compositions and Methods
; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/016,481
; CURRENT FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-481-3

Query Match 100.0%; Score 498; DB 13; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.6e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AVITGACRDRVCGAGTCCATSLWLRGLRMCTPLRGEGECHPGSHKVPFFRKXHTCP 60
Db 1 AVITGACRDRVCGAGTCCATSLWLRGLRMCTPLRGEGECHPGSHKVPFFRKXHTCP 60
Qy 61 CLPNLLCSRFDPGRYRCMDLKNINF 86
Db 61 CLPNLLCSRFDPGRYRCMDLKNINF 86

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RESULT 2
US-10-323-157-3
; Sequence 3, Application US/10323157
; Publication No. US20030113867A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Ehler, Frederick
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; TITLE OF INVENTION: Compositions and Methods
; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/323,157
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/10/016,481
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-323-157-3

Query Match      100.0%; Score 498; DB 14; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.6e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVCGAGTCCCAISLWRLGLRMCTPLGREGECHPGSHKVPFFFRKRKHHTCP 60
Db 1 AVITGACERDVCGAGTCCCAISLWRLGLRMCTPLGREGECHPGSHKVPFFFRKRKHHTCP 60

QY 61 CLPNLLCSRFDPGRYRCSDMLKNINF 86
Db 61 CLPNLLCSRFDPGRYRCSDMLKNINF 86

RESULT 3
US-10-417-426-9
; Sequence 9, Application US/10417426
; Publication No. US2003023535A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Bullock, Clayton M.
; TITLE OF INVENTION: Screening and Therapeutic Methods For
; TITLE OF INVENTION: Treating Circadian Rhythm Disorders
; FILE REFERENCE: P-UC 5773
; CURRENT APPLICATION NUMBER: US/10/417,426
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: US 60/372,836
; PRIOR FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-417-426-9

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Best Local Similarity 100.0%; Pred. No. 2.6e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AVITGACERDVCGAGTCCCAISLWRLGLRMCTPLGREGECHPGSHKVPFFFRKRKHHTCP 60

QY 61 CLPNLLCSRFDPGRYRCSDMLKNINF 86
Db 61 CLPNLLCSRFDPGRYRCSDMLKNINF 86
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RESULT 4
US-10-333-192-21
; Sequence 21, Application US/10333192
; Publication No. US2004007535A1
; GENERAL INFORMATION:
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: TAKATSU, Yoshihiro
; APPLICANT: WATANABE, Takuya
; APPLICANT: TERAOKA, Yasuko
; APPLICANT: SHINTANI, Yasushi
; APPLICANT: HINUMA, Syuji
; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof
; FILE REFERENCE: 2762USOP
; CURRENT APPLICATION NUMBER: US/10/333,192
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: JP 2000-217442
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: JP 2001-26779
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/JPO1/06162
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 21
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Human
US-10-333-192-21

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Best Local Similarity 100.0%; Pred. No. 2.6e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AVITGACERDVCGAGTCCCAISLWRLGLRMCTPLGREGECHPGSHKVPFFFRKRKHHTCP 60

QY 61 CLPNLLCSRFDPGRYRCSDMLKNINF 86
Db 61 CLPNLLCSRFDPGRYRCSDMLKNINF 86

RESULT 5
US-10-680-554-5
; Sequence 5, Application US/10680554
; Publication No. US20040229291A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Cheng, Michelle Y.
; TITLE OF INVENTION: Screening and Therapeutic Methods
; TITLE OF INVENTION: Relating to Neurogenesis
; FILE REFERENCE: 66778-356
; CURRENT APPLICATION NUMBER: US/10/680,554
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: US 60/416,202
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-680-554-5

Query Match      100.0%; Score 498; DB 16; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.6e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVCGAGTCCCAISLWRLGLRMCTPLGREGECHPGSHKVPFFFRKRKHHTCP 60
Db 1 AVITGACERDVCGAGTCCCAISLWRLGLRMCTPLGREGECHPGSHKVPFFFRKRKHHTCP 60

QY 61 CLPNLLCSRFDPGRYRCSDMLKNINF 86
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Db 61 CLPILLCSEFPDGRYRCMDLKNINF 86

RESULT 6

US-10-713-567-3
; Sequence 3, Application US/10713567
; Publication NO. US20040235732A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Ehler, Frederick J.
; TITLE OF INVENTION: Methods For Modulating Angiogenesis
; TITLE OF INVENTION: Methods For Modulating Angiogenesis
; FILE REFERENCE: 66778-359
; CURRENT APPLICATION NUMBER: US/10/713,567
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/426,203
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 10/ 016,481
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-713-567-3

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Best Local Similarity 100.0%; Pred. No. 2.6e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVCGAGTCCCAISLWRLGLRMCTPLGREGECHPGSHKVPFFRKRKHTCP 60
Db 1 AVITGACERDVCGAGTCCCAISLWRLGLRMCTPLGREGECHPGSHKVPFFRKRKHTCP 60
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Db 61 CLPILLCSEFPDGRYRCMDLKNINF 86

RESULT 7

US-10-811-328-3
; Sequence 3, Application US/10811328
; Publication NO. US20050026828A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Methods For Modulating Gastric Secretion
; TITLE OF INVENTION: Using Prokineticin Receptor Antagonists
; FILE REFERENCE: 66778-365
; CURRENT APPLICATION NUMBER: US/10/811,328
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: 60/457,891
; PRIOR FILING DATE: 2003-03-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-811-328-3

Query Match 100.0%; Score 498; DB 17; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.6e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVCGAGTCCCAISLWRLGLRMCTPLGREGECHPGSHKVPFFRKRKHTCP 60
Db 1 AVITGACERDVCGAGTCCCAISLWRLGLRMCTPLGREGECHPGSHKVPFFRKRKHTCP 60
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Db 61 CLPILLCSEFPDGRYRCMDLKNINF 86

RESULT 8

US-10-912-907-3
; Sequence 3, Application US/10912907
; Publication NO. US20050037464A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Ehler, Frederick
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; TITLE OF INVENTION: Compositions and Methods
; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/912,907
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US/10/016,481
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-912-907-3

Query Match 100.0%; Score 498; DB 17; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.6e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVCGAGTCCCAISLWRLGLRMCTPLGREGECHPGSHKVPFFRKRKHTCP 60
Db 1 AVITGACERDVCGAGTCCCAISLWRLGLRMCTPLGREGECHPGSHKVPFFRKRKHTCP 60
QY 61 CLPILLCSEFPDGRYRCMDLKNINF 86
Db 61 CLPILLCSEFPDGRYRCMDLKNINF 86

RESULT 9

US-10-415-724-3
; Sequence 3, Application US/10415724
; Publication NO. US20050074758A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; TITLE OF INVENTION: Compositions and Methods
; FILE REFERENCE: P-UC 5030
; CURRENT APPLICATION NUMBER: US/10/415,724
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-415-724-3

Query Match 100.0%; Score 498; DB 17; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.6e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVCGAGTCCCAISLWRLGLRMCTPLGREGECHPGSHKVPFFRKRKHTCP 60
Db 1 AVITGACERDVCGAGTCCCAISLWRLGLRMCTPLGREGECHPGSHKVPFFRKRKHTCP 60
QY 61 CLPILLCSEFPDGRYRCMDLKNINF 86
Db 61 CLPILLCSEFPDGRYRCMDLKNINF 86

Db 61 CLPNLLCSRFPDGRYRCSDMLKNINF 86

RESULT 14

US-10-503-554A-81
; Sequence 81, Application US/10503554A
; Publication No. US20050176632A1
; GENERAL INFORMATION:
; APPLICANT: OHTAKI, TETSUYA
; APPLICANT: MASUDA, YASUSHI
; APPLICANT: TAKATSU, YOSHIHIRO
; TITLE OF INVENTION: ANGIOGENESIS INHIBITORS
; FILE REFERENCE: 61807 (46342)
; CURRENT APPLICATION NUMBER: US/10/503,554A
; PRIOR FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: JP2002-27299
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 81
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-503-554A-81

Query Match 99.8%; Score 497; DB 18; Length 86;
Best Local Similarity 98.8%; Pred. No. 3.3e-45;
Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCCAISLWLGLRMCTPLGREGEGCHPGSHKVPFFRKRKHTTCTP 60

Db 1 AVITGACERDVQCGAGTCCCAISLWLGLRMCTPLGREGEGCHPGSHKVPFFRKRKHTTCTP 60

QY 61 CLPNLLCSRFPDGRYRCSDMLKNINF 86

Db 61 CLPNLLCSRFPDGRYRCSDMLKNINF 86

RESULT 15

US-10-016-481-16
; Sequence 16, Application US/10016481
; Publication No. US20020115610A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; TITLE OF INVENTION: Compositions and Methods
; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/016,481
; CURRENT FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-016-481-16

Query Match 99.2%; Score 494; DB 13; Length 85;
Best Local Similarity 100.0%; Pred. No. 6.8e-45;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VITGACERDVQCGAGTCCCAISLWLGLRMCTPLGREGEGCHPGSHKVPFFRKRKHTTCTP 61

Db 1 VITGACERDVQCGAGTCCCAISLWLGLRMCTPLGREGEGCHPGSHKVPFFRKRKHTTCTP 60

QY 62 LPNLLCSRFPDGRYRCSDMLKNINF 86

Db 61 LPNLLCSRFPDGRYRCSDMLKNINF 85

Search completed: November 1, 2005, 15:26:42
Job time : 165 secs

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